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OM protein - protein search, using sw model

Run on: January 10, 2002, 15:34:02 ; Search time 23.93 Seconds
(Without alignments)
256,919 Million cell updates/sec

Title: US-09-555-534-2

Perfect score: 476
Sequence: 1 EPVDPRLERPMKHPGSGPMTA.....VLSKQPTSGSGDPTGPK 83

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

A.Geneseq_1101.*
1: /SIDSR/gcgdata/geneseq/genesqp/AA1980.DAT.*
2: /SIDSR/gcgdata/geneseq/genesqp/AA1981.DAT.*
3: /SIDSR/gcgdata/geneseq/genesqp/AA1982.DAT.*
4: /SIDSR/gcgdata/geneseq/genesqp/AA1983.DAT.*
5: /SIDSR/gcgdata/geneseq/genesqp/AA1984.DAT.*
6: /SIDSR/gcgdata/geneseq/genesqp/AA1985.DAT.*
7: /SIDSR/gcgdata/geneseq/genesqp/AA1986.DAT.*
8: /SIDSR/gcgdata/geneseq/genesqp/AA1987.DAT.*
9: /SIDSR/gcgdata/geneseq/genesqp/AA1988.DAT.*
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13: /SIDSR/gcgdata/geneseq/genesqp/AA1992.DAT.*
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15: /SIDSR/gcgdata/geneseq/genesqp/AA1994.DAT.*
16: /SIDSR/gcgdata/geneseq/genesqp/AA1995.DAT.*
17: /SIDSR/gcgdata/geneseq/genesqp/AA1996.DAT.*
18: /SIDSR/gcgdata/geneseq/genesqp/AA1997.DAT.*
19: /SIDSR/gcgdata/geneseq/genesqp/AA1998.DAT.*
20: /SIDSR/gcgdata/geneseq/genesqp/AA1999.DAT.*
21: /SIDSR/gcgdata/geneseq/genesqp/AA2000.DAT.*
22: /SIDSR/gcgdata/geneseq/genesqp/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	476	100.0	83	20	AAV22958	Wild type Tat amin
2	465	97.7	86	8	AAV70598	HIV virus recombin
3	465	97.7	86	10	AAV91903	Tat protein derive
4	465	97.7	86	10	AAV91905	CDNA for tat prote
5	465	97.7	86	10	AAV93140	Synthetic TAR prot
6	465	97.7	86	14	AAV38618	Sequence of the HI
7	465	97.7	86	17	AAV86625	HIV TAR. Human im
8	465	97.7	86	18	AAV31202	Human Immunodefici
9	465	97.7	86	18	AAV26443	HIV tat protein.
10	465	97.7	86	19	AAV71385	Amino acid sequenc
11	465	97.7	86	19	AAV76148	HIV Type I TAR pro

12	465	97.7	86	21	AAV96881	Human immunodefici
13	465	97.7	87	12	AAV13379	TAT protein. Synt
14	465	97.7	95	20	AAV02350	A representative H
15	465	97.7	95	22	AAV63232	Amino acid sequenc
16	465	97.7	302	20	AAV02351	A representative H
17	465	97.7	302	22	AAV63233	Amino acid sequenc
18	465	97.7	411	20	AAV02353	A representative L
19	465	97.7	411	22	AAV63235	Amino acid sequenc
20	465	97.7	413	20	AAV02355	A representative L
21	465	97.7	413	22	AAV63237	Amino acid sequenc
22	459	96.4	86	20	AAV22960	Lys41 mutant tat a
23	453	95.2	86	20	AAV22959	Cys22 mutant tat a
24	452	95.0	95	20	AAV02356	A representative H
25	452	95.0	95	22	AAV63238	Amino acid sequenc
26	452	95.0	302	20	AAV02357	A representative H
27	452	95.0	302	22	AAV63239	Amino acid sequenc
28	449	94.3	86	11	AAV02227	Sequence of the tr
29	449	94.3	86	16	AAV87742	Wild type TAT HIV
30	438	92.0	86	15	AAV48966	Diversified HIV-1
31	438	92.0	86	15	AAV57346	Peptide fragment o
32	436.5	91.7	83	20	AAV22961	RGD-delta mutant t
33	435	91.4	86	21	AAV10050	HIV-1 tat protein.
34	433	91.0	86	15	AAV48964	Full length TAR.
35	433	91.0	86	22	AAV64257	Human protein: Seq
36	430.5	90.4	83	20	AAV22962	Lys41-RGD-delta mu
37	429	90.1	86	22	AAV46679	HIV-1 Tat peptide
38	429	90.1	86	22	AAV46685	HIV-1 tat peptide
39	420	88.2	86	16	AAV77542	Trans-dominant var
40	413	86.8	101	21	AAV14224	HIV Tat_SFI62. Hu
41	401	84.2	102	21	AAV14225	HIV Tat_Cys22_SF16
42	397	83.4	101	12	AAV12259	HIV-1 strain OYI T
43	397	83.4	101	21	AAV30514	Sequence of the ta
44	394	82.8	86	22	AAV46681	HIV-1 Tat peptide
45	388	81.5	72	7	AAV60699	Trans-acting trans

ALIGNMENTS

RESULT 1
AAV22958
ID AAV22958 standard; Protein: 83 AA.
XX
AC AAV22958;
XX
DT 20-AUG-1999 (first entry)
XX
DE Wild type Tat amino acid sequence of HIV-1.
XX
KW HIV tat protein; AIDS; tumour; HIV infection; dendritic cell;
KW Kaposi's sarcoma cell; activated endothelial cell;
KW cytokine-activated endothelial cell; vaccine.
XX
OS Human immunodeficiency virus type 1.
XX
PN WO9927958-A2.
XX
PD 10-JUN-1999.
XX
PF 30-NOV-1998; 98WO-EP07721.
XX
PR 01-DEC-1997; 97IR-RM00743.
XX
PA (SUPE-) INST SUPERIORE DI SANITA.
XX
PI Enso11 B;
XX
DR WPI: 1999-385324/32.
DR N-PSDB; AAV81354.
XX
PT Use of biologically active HIV Tat protein, fragments or mutants
XX
PS Claim 8; Page 116; 150pp; English.

XX The present sequence represents tat protein. The specification describes
 CC the use of biologically active HIV tat protein, fragments or mutants
 CC for the prophylactic or therapeutic treatment of AIDS and tumours,
 CC syndromes and symptoms associated with HIV infection. A biologically
 CC active Tat protein, fragments and/or mutants and/or Tat DNA which is
 CC capable of entering and localizing in the nuclei of activated endothelial
 CC cells or dendritic cells and/or activating the proliferation, migration
 CC and invasion of Kaposi's sarcoma (KS) cells and cytokine-activated
 CC endothelial cells, is used as a vaccine. HIV-1 tat or its mutants
 CC in a biologically active form is able to induce a very strong immune
 CC response against HIV, able to prevent infection or the development of
 CC the disease and to permit efficient therapeutic strategies in
 CC HIV-1-infected individuals.
 XX
 SQ Sequence 83 AA:

Query Match 100.0%; Score 476; DB 20; Length 83;
 Best Local Similarity 100.0%; Pred. No. 8.8e-43;
 Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EPVDRLEPMKHPGSOPTACTNCCYCKCCFHCQVCFITKALSYGKKRRRRPPGSG 60
 DB 1 epvdrlepmkhpqsgpactnccyckccfhcqvcfilitkalsygrkrrrrppgsg 60
 OY 61 THQVSLSKOPTSOSRQDPTGPKE 83
 DB 61 thqvslskqptsqsrqdpptgpke 83

RESULT 2

AAP70598
 ID AAP70598 standard; protein; 86 AA.

XX AAP70598;

XX 17-MAR-1991 (first entry)

DE HIV virus recombinant tat-3 protein.

KW HIV virus; tat-3 protein; plasmid pAS1; plasmid pOTS-tatIIID;
 KW plasmid pOTS-tatIII; AIDS; vaccine.

XX Escherichia coli.

XX W08702989-A.

XX 21-MAY-1987.

XX 05-NOV-1986; 86WO-US02374.

XX 06-NOV-1985; 85US-0795559.

XX (SMIK) SMITHKLINE BECKMAN CORP.

XX (USDC) US DEPT COMMERCE.

PI Aldovinnl A, Debouck CM, Rosenberg C, Wong-Staal F;

DR WPI: 1987-150612/21.

DR N-PSDB: AAN70948.

PT Recombinant TAT-3 gene of HTLV-III - for producing polypeptide(s)
 PT for use in detection vaccination purification and therapy involving
 PT HTLV-III infection.

PS Claim 2; Page 14; 20pp; English.

XX The sequence encodes the HIV virus tat-3 protein. The DNA
 CC sequence encoding this protein is present in E. coli
 CC plasmids pAS1, pOTS-tatIIID or pOTS-tatIII. Recombinant
 CC tat-3 protein and its derivatives can be used in the
 CC detection and therapy of HIV virus infection as well as an

CC an antigenic component of a vaccine.
 XX
 SQ Sequence 86 AA:

Query Match 97.7%; Score 465; DB 8; Length 86;
 Best Local Similarity 97.6%; Pred. No. 1.3e-41;
 Matches 83; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

OY 1 EPVDRLEPMKHPGSOPTACTNCCYCKCCFHCQVCFITKA--ISYGRKKRRRRPPG 58
 DB 2 epvdrlepmkhpqsgpactnccyckccfhcqvcfilitkalsygrkrrrrppg 61
 OY 59 SOTHQVSLSKOPTSOSRQDPTGPKE 83
 DB 62 sqthqvslskqptsqsrqdpptgpke 86

RESULT 3

AAP91903
 ID AAP91903 standard; protein; 86 AA.

XX AAP91903;

XX 12-MAY-1990 (first entry)

DE Tat protein derived from human immuno-deficiency virus

DE (HIV: HTLV-III/LAV) cDNA.

KW Recombinant vaccinia virus; HIV tat protein cDNA; HTLV-III;
 KW LAV; AIDS; ARC.

XX Human immunodeficiency virus.

XX JF01085072-A.

XX 30-MAR-1989.

XX 25-SEP-1987; 87JP-0240514.

XX 25-SEP-1987; 87JP-0240514.

XX (KOKU-) KOKURITSU YOBO EISE (JAPG).

XX WPI: 1989-140769/19.

XX N-PSDB: AAN92430.

PT Recombinant vaccinia virus
 PT - has protein coding complementary DNA from human
 PT immuno-deficiency virus in genome DNA domain

XX Fig 4; page 420; 8pp; Japanese.

CC All or part of it can be produced by recombinant vaccinia virus by
 CC integrating it into the genome region nonessential for vaccinia virus
 CC proliferation and then infecting animal cells with the recombinant virus.
 CC Tat protein can be used to diagnose HIV infection and for prophylaxis
 CC for AIDS or ARC patients. It can also be used to develop a live vaccine
 CC using temperature-sensitive Lister strain of vaccinia virus.

XX Sequence 86 AA;

Query Match 97.7%; Score 465; DB 10; Length 86;
 Best Local Similarity 97.6%; Pred. No. 1.3e-41;
 Matches 83; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

OY 1 EPVDRLEPMKHPGSOPTACTNCCYCKCCFHCQVCFITKA--ISYGRKKRRRRPPG 58
 DB 2 epvdrlepmkhpqsgpactnccyckccfhcqvcfilitkalsygrkrrrrppg 61
 OY 59 SOTHQVSLSKOPTSOSRQDPTGPKE 83
 DB 62 sqthqvslskqptsqsrqdpptgpke 86

PF 11-DEC-1992; 92WO-US10770.
 XX
 PR 13-DEC-1991; 91US-0808452.
 PR 21-JAN-1992; 92US-0826934.
 XX
 PA (STRI) SRI INT.
 XX
 PI Jayasena SD, Johnston BH;
 XX
 DR WPI: 1993-214176/26.
 XX
 XX
 PT Viral polypeptide(s) with site-specific RNA binding - contain
 PT moiety to cleave RNA backbone and are used to inhibit HIV antigen
 PT expression in infected cells
 XX
 PS Claim 2; Figure 2A; 94pp; English.
 XX
 CC TAT is a potent transactivator of long terminal repeat (LTR)-
 CC directed viral gene expression. TAT-induced transactivation requires
 CC the present of the TAR (transactivation response) element, located
 CC at the 5'UTR of the viral RNA element. The sequence of RNA target
 CC molecules were chosen based on previous studies characterising the
 CC binding properties of the HIV-encoded TAT protein and the TAR target
 CC region from both HIV-1 and HIV-2. HIV-1 TAR is the 57-nt RNA stem-
 CC loop structure found in HIV-1 mRNA (nt 1-57). The RNA substrate is
 CC given in AA044139.
 XX
 SO Sequence 86 AA;

Query Match 97.7%; Score 465; DB 14; Length 86;
 Best Local Similarity 97.6%; Pred. No. 1.3e-41;
 Matches 83; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

OY 1 EPVDPRLPEPMKHPGSOPTACTNCYCKKCFHCQYCFITKA--ISYGRKKRRRRRRPQG 58
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 2 epvdpriepwkhpgsqpktaactncycckcchgcqvcftlkalgisygkrkrrrrppqg 61
 OY 59 SOTHQVSLSKOPTSOSRQDPTGPKE 83
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 62 sqthqvslskqptsqsrqdpqpkpe 86

RESULT 7
 AAR86625
 ID AAR86625 standard; Protein; 86 AA.
 XX
 AC AAR86625;
 XX
 DT 28-JUN-1996 (first entry)
 XX
 DE HIV TAT.
 XX
 KW Immunogen; cellular uptake region; transactivating protein; TAT; HIV;
 KW viraemia; antibody.
 XX
 OS Human immunodeficiency virus.
 XX
 FH Key Location/Qualifiers
 FT Peptide 46..63
 FT /note= "Cellular uptake region"
 XX
 PN WO9531999-A1.
 XX
 PD 30-NOV-1995.
 XX
 PE 16-MAY-1995; 95WO-US06077.
 XX
 PR 23-MAY-1994; 94US-0247991.
 XX
 PR (IMMU-) IMMUNOGIOLOGY RES INST INC.
 PA
 PI Culler MD, Goldstein G, Shenbagamurthi P;

XX
 DR WPI: 1996-049298/05.
 DR N-PSDB: AAT06634.
 XX
 PT Immunogen containing cellular uptake region of viral TAT protein -
 PT induces high antibody titre against TAT, partic. for preventing or
 PT treating HIV infection
 XX
 PS Disclosure; Figure 1; 54pp; English.
 XX
 CC This sequence represents the HIV transactivating protein, TAT. The
 CC sequences given in AAR86601-19 are immunogens derived from the cellular
 CC uptake region of this protein. These peptides are based on the region
 CC comprising amino acids 46-63. The immunogenic peptides are used to
 CC protect against infection by HIV. They may also be used to reduce
 CC viraemia in already infected patients. These immunogens may be used
 CC to identify, or generate, antibodies specific for TAT.
 XX
 SO Sequence 86 AA;

Query Match 97.7%; Score 465; DB 17; Length 86;
 Best Local Similarity 97.6%; Pred. No. 1.3e-41;
 Matches 83; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

OY 1 EPVDPRLPEPMKHPGSOPTACTNCYCKKCFHCQYCFITKA--ISYGRKKRRRRRRPQG 58
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 2 epvdpriepwkhpgsqpktaactncycckcchgcqvcftlkalgisygkrkrrrrppqg 61
 OY 59 SOTHQVSLSKOPTSOSRQDPTGPKE 83
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 62 sqthqvslskqptsqsrqdpqpkpe 86

RESULT 8
 AAW31202
 ID AAW31202 standard; protein; 86 AA.
 XX
 AC AAW31202;
 XX
 DT 20-MAR-1998 (first entry)
 XX
 DE Human Immunodeficiency Virus Type 1 Tat protein.
 XX
 KW Human immunodeficiency virus; HIV Type 1; Tat protein;
 KW cargo molecules; intracellular delivery; fusion protein;
 KW therapeutic; prophylactic; diagnostic; transport polypeptide.
 XX
 OS Human immunodeficiency virus type 1.
 XX
 FH Key Location/Qualifiers
 FT Region 22..36
 FT /label= cysteine_rich
 FT Region 49..57
 FT /label= basic_region
 FT Domain 73..86
 FT /label= carboxy_terminal_domain
 XX
 PN US5674980-A.
 XX
 PD 07-OCT-1997.
 XX
 PF 21-DEC-1989; 89US-0454450.
 XX
 XX 28-APR-1994; 94US-0235403.
 PR 21-DEC-1989; 89US-0454450.
 PR 02-JAN-1991; 91US-0636662.
 PR 21-AUG-1992; 92US-0934375.
 PR 19-AUG-1993; 93WO-US07833.
 PR 24-NOV-1993; 93US-0158015.
 PR 25-MAY-1995; 95US-0450098.
 XX
 PA (BARS/) BARSQUM J G.

PA (FAME/) FAMELL S E.
 PA (FRAN/) FRANKEL A.
 PA (PABO/) PABO.
 PA (PEPI/) PEPIISKY R B.
 PI Barsom JG, Fawell SE, Frankel A, Pabo C, Pepinsky RB;
 XX WPI; 1997-502388/46.
 XX
 PT Fusion proteins containing truncated HIV tat sequences - useful for
 PT intracellular delivery of viral repressor proteins
 PS
 PS Example I; Fig 1; 77pp; English.
 XX
 CC This sequence represents the tat protein from Human Immunodeficiency
 CC virus, Type 1 which can be used in a novel method for the delivery of
 CC biologically active cargo molecules into the cytoplasm and nuclei of
 CC eukaryotic cells. The tat protein from immunodeficiency virus (e.g.
 CC HIV-1, HIV-2, SIV) is readily taken up into cells when present
 CC extracellularly. By modifying the HIV tat protein i.e. removing the
 CC cytosine-rich region and the carboxy-terminal domain and covalently
 CC linking the protein to a cargo molecule to form a fusion protein,
 CC the problems of spurious trans-activation and disulphide aggregation are
 CC eradicated. The reduced size of transport polypeptides also minimises
 CC interference with the biological activity of the cargo molecule. This is
 CC applicable for therapeutic, prophylactic or diagnostic intracellular
 CC delivery of small molecules and macromolecules e.g. proteins, nucleic
 CC acids and polysaccharides.
 XX
 SQ Sequence 86 AA:
 Query Match 97.7%; Score 465; DB 18; Length 86;
 Best Local Similarity 97.6%; Pred. No. 1.3e-41;
 Matches 83; Conservative 0; Mismatches 0; Indels 2; Gaps 1;
 QY 1 EPVDPRLPEPMKHPGSGPACTACTNCYCKKCCFHCQVCFITKA--ISYGRKKRRQRRRPPG 58
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 2 epvdprlepwmkhpqsgpactactncycckcchqvcfiktalglsygrkrrrrppg 61
 QY 59 SOTHQVSLSKOPTSOSRDPPTGPK 83
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 62 sqthqvslskqpsgrgdptgpke 86
 RESULT 9
 AAW26443
 ID AAW26443 standard; Protein: 86 AA.
 XX
 AC AAW26443;
 XX
 DT 16-DEC-1997 (first entry)
 XX
 DE HIV tat protein.
 XX
 XX HIV; tat protein; transport protein; cargo delivery.
 XX
 OS Human immunodeficiency virus type 1.
 XX
 FH Key Location/Qualifiers
 FT Region 23..36
 FT /label= Cys-rich_region
 FT 47..59
 FT /label= Basic_region
 FT 73..86
 FT /label= C-terminal
 FT Region
 XX
 XX US5652122-A.
 XX
 XX 29-JUL-1997.
 XX
 XX 21-DEC-1989; 89US-0454450.
 XX

PR 28-APR-1994; 94US-0235403.
 PR 21-DEC-1989; 89US-0454450.
 PR 02-JAN-1991; 91US-0636662.
 PR 21-AUG-1992; 92US-0934375.
 PR 19-AUG-1993; 93WO-0507833.
 PR 24-NOV-1993; 93US-0158015.
 PR 25-MAY-1995; 95US-0450257.
 XX
 PA (BARS/) BARSOM J G.
 PA (FAME/) FAMELL S E.
 PA (FRAN/) FRANKEL A.
 PA (PABO/) PABO C.
 PA (PEPI/) PEPIISKY R B.
 XX
 PI Barsom JG, Fawell SE, Frankel A, Pabo C, Pepinsky RB;
 XX WPI; 1997-392943/36.
 XX
 DR New DNA constructs for transporting molecules to cells - encode a
 PT fusion protein comprising a modified HIV tat protein and a
 PT carboxy-terminal cargo moiety
 PS
 PS Disclosure; Fig 1; 76pp; English.
 XX
 CC This polypeptide comprises the HIV tat protein. Novel transport
 CC proteins comprise modified HIV tat covalently attached to a cargo
 CC molecule (see AAW26436-42). The modified tat protein (see AAW26444-49)
 CC is characterised by the presence of the tat basic region (thought
 CC to be required for nuclear localisation), and the absence of the
 CC Cys-rich region and the exon 2-encoded C-terminal region. These
 CC modifications solve the potential problems of spurious
 CC trans-activation and disulphide aggregation, while the reduced size
 CC of the transport proteins minimises interference with the
 CC biological activity of the cargo molecule. DNA molecules that
 CC encode the modified tat fusion proteins are claimed and can be
 CC used to deliver polypeptides or nucleic acids to the cytoplasm
 CC of nuclei of cells in vivo or in vitro.
 XX
 SQ Sequence 86 AA:
 Query Match 97.7%; Score 465; DB 18; Length 86;
 Best Local Similarity 97.6%; Pred. No. 1.3e-41;
 Matches 83; Conservative 0; Mismatches 0; Indels 2; Gaps 1;
 QY 1 EPVDPRLPEPMKHPGSGPACTACTNCYCKKCCFHCQVCFITKA--ISYGRKKRRQRRRPPG 58
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 2 epvdprlepwmkhpqsgpactactncycckcchqvcfiktalglsygrkrrrrppg 61
 QY 59 SOTHQVSLSKOPTSOSRDPPTGPK 83
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 62 sqthqvslskqpsgrgdptgpke 86
 RESULT 10
 AAW71385
 ID AAW71385 standard; Protein: 86 AA.
 XX
 AC AAW71385;
 XX
 DT 04-DEC-1998 (first entry)
 XX
 DE Amino acid sequence of HIV Tat 85.
 XX
 XX HIV tat 85; leaderless protein; inhibition; export; angiogenesis;
 KW restenosis; treatment; tumour; inflammation; cell proliferation;
 KW diabetes; retinopathy; infection; polycystic kidney disease;
 KW atherosclerosis.
 XX
 XX Human immunodeficiency virus.
 XX
 XX WO9837880-A1.
 XX

PD 03-SEP-1998.
 XX 25-FEB-1998; 98WO-US03689.
 PF 26-FEB-1997; 97US-0807014.
 XX (CIBL-) CIBLEX CORP.
 PA Baird A, Florikiewicz RZ;
 XX WPI: 1998-495377/42.
 DR N-PSDB; AAV60345.
 XX
 PT Inhibiting export of leaderless protein with agent that inhibits
 PT binding to transporter protein - especially for treating
 PT angiogenesis and restenosis by preventing export of fibroblast
 PT growth factor; also methods for identifying leaderless proteins and
 PT their transporters
 PS
 PS Claim 2; Page 70; 116pp; English.
 XX
 CC The present sequence represents Human immunodeficiency virus (HIV) Tat
 CC 85, a leaderless protein. A leaderless protein refers to a protein that
 CC is found in an extracellular environment, but lacks a canonical leader
 CC sequence. The specification describes a method for inhibiting export of
 CC a leaderless protein from a cell. The method comprises treating
 CC the cell with an agent that inhibits binding between the leaderless
 CC protein and a transport molecule. Treatment with the inhibiting agent
 CC is specifically used to treat angiogenesis and restenosis, i.e. where
 CC expression of FGF-2 is inhibited, and the agent is applied to endothelial
 CC or smooth muscle cells. Other applications are treatment of tumors
 CC (melanoma, teratocarcinoma, ovarian carcinoma, bladder cancer and
 CC neuroblastoma), inflammation, cell proliferation, complications of
 CC diabetes (e.g. retinopathy), viral, bacterial or fungal infections,
 CC polycystic kidney disease and atherosclerosis.
 XX
 SQ Sequence 86 AA;

Query Match 97.7%; Score 465; DB 19; Length 86;
 Best Local Similarity 97.6%; Pred. No. 1.3e-41;
 Matches 83; Conservative 0; Mismatches 0; Indels 2; Gaps 1;
 QY 1 EPVDRLEPRWKHPGSPRTACTNCYCKKCCFHCQVCFTTKA--ISYGRKKRRRRRPPQG 58
 Db 2 EPVDRLEPRWKHPGSPRTACTNCYCKKCCFHCQVCFTTKA--ISYGRKKRRRRRPPQG 61
 QY 59 SOTHQVSLSKOPTSOSRSDPTGPKK 83
 Db 62 sqthqvsiskqptsqsrqdpkpke 86
 Db
 RESULT 11
 AAW76148
 ID AAW76148 standard; protein; 86 AA.
 XX
 AC AAW76148;
 XX
 DT 24-NOV-1998 (first entry)
 XX
 DE HIV Type I Tat protein.
 XX
 KW Tat protein; cargo molecule; therapy; diagnosis; transport protein;
 KW fusion protein; human papillomavirus E2 repressor; target cell.
 XX
 OS Human immunodeficiency virus type 1.
 XX
 PN US5804604-A.
 XX
 PD 08-SEP-1998.
 XX
 PF 25-MAY-1995; 95US-0450236.
 XX

PR 28-APR-1994; 94US-0235403.
 PR 21-DEC-1989; 89US-0454450.
 PR 02-JAN-1991; 91US-0636662.
 PR 19-AUG-1993; 93WO-US07833.
 PR 24-NOV-1993; 93US-0156015.
 PR 25-MAY-1995; 95US-0450236.
 XX
 PA (BIOJ) BIOGEN INC.
 XX
 PI Barsom JG, Fawell SE, Frankel A, Pabo C, Pepinsky RB;
 XX WPI: 1998-505702/43.
 DR
 XX
 PT HIV tat-derived transport fusion proteins - used to deliver
 PT biological active molecules e.g. peptides) or nucleic acids,
 PT specifically into cytoplasm or nuclei of cells
 PS
 PS Disclosure: Fig 1; 83pp; English.
 XX
 CC This sequence represents the human immunodeficiency virus (HIV) Type I
 CC Tat protein which is used in a method for the delivery of biologically
 CC active cargo molecules into the cytoplasm and nuclei of cells, for
 CC therapeutic, prophylactic or diagnostic purposes. This is accomplished
 CC by the presence of a small, basic section of tat transport protein of
 CC HIV. This is used as it is this protein which is observed to cause human
 CC cells in culture to take up HIV. The method involves the use of a cargo
 CC moiety in combination with a transport moiety usually in the form of a
 CC fusion protein. The cargo moiety is a human papillomavirus E2 repressor
 CC that retains its biological activity after delivery into a target cell
 CC and where the transport moiety is one of following HIV tat protein
 CC fragments (a) aa 47-58, (b) aa 47-72, (c) 38-72, (d) aa 38-58, (e)
 CC aa 37-58, (f) aa 1-21 and 38-72, (g) aa 47-62 or aa 38-62. The proteins
 CC allow delivery of specific peptides into cells at high concentrations
 CC due to use of existing transporters. Previous methods of delivery
 CC include bombardment and transforming, which only allow a fraction of the
 CC cell population to be infected and can additionally damage cells as
 CC they cause physical opening of the cell walls/membranes to allow entry.
 XX
 SQ Sequence 86 AA;

Query Match 97.7%; Score 465; DB 19; Length 86;
 Best Local Similarity 97.6%; Pred. No. 1.3e-41;
 Matches 83; Conservative 0; Mismatches 0; Indels 2; Gaps 1;
 QY 1 EPVDRLEPRWKHPGSPRTACTNCYCKKCCFHCQVCFTTKA--ISYGRKKRRRRRPPQG 58
 Db 2 EPVDRLEPRWKHPGSPRTACTNCYCKKCCFHCQVCFTTKA--ISYGRKKRRRRRPPQG 61
 QY 59 SOTHQVSLSKOPTSOSRSDPTGPKK 83
 Db 62 sqthqvsiskqptsqsrqdpkpke 86
 Db
 RESULT 12
 AAY96881
 ID AAY96881 standard; Protein; 86 AA.
 XX
 AC AAY96881;
 XX
 DT 31-OCT-2000 (first entry)
 XX
 DE Human immunodeficiency virus Tat 85.
 XX
 KW Human immunodeficiency virus; HIV; Tat 85; transport molecule; go1gi;
 KW leaderless; endoplasmic reticulum; protein export; detection; inhibitor.
 XX
 OS Human immunodeficiency virus type 1.
 XX
 PN
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 53
 FT Misc-difference 53
 FT Misc-difference 80
 FT Misc-difference 80

FT /note= "Encoded by GAA"
 XX US6083706-A.
 XX 04-JUL-2000.
 PD
 XX 25-FEB-1998; 98US-0030613.
 PF
 XX 26-FEB-1997; 97US-0807014.
 PR
 XX (CIBL-) CIBLEX CORP.
 PA
 XX Baird A, Florkiewicz RZ;
 PI
 XX WPI: 2000-464338/40.
 DR
 XX N-PSDB; AAA53572.
 DR
 XX
 PT Detecting transport molecules, useful for identifying proteins that
 PT mediate leaderless protein export across cell membranes, by contacting
 PT cell extracts with a fusion protein of leaderless protein and a tag to
 PT form a complex
 PT
 XX
 PS Disclosure; Column 55-56; 64pp; English.
 XX
 CC Detecting a transport molecule involved in non-endoplasmic reticulum
 CC (ER)/Golgi leaderless protein export, comprises contacting test cell
 CC extracts or membranes with a fusion protein of a leaderless protein and
 CC a tag to form a complex of the fusion protein bound to the transport
 CC molecule, and detecting the transport molecule in an isolated complex.
 CC The leaderless protein is a protein found in the extracellular
 CC environment that lacks a canonical leader sequence, interleukin (IL)
 CC 1-alpha, or 1-beta, fibroblast growth factor (FGF) 1 or 2, human
 CC immunodeficiency virus (HIV) tat, platelet-derived endothelial cell
 CC growth factor (PD-ECGF), ciliary neurotrophic factor (CNTF), sciatic
 CC nerve growth-promoting activity, vas deferens protein, transglutaminase,
 CC L-14 lectin, factor XIIIa, thiodoxin-like protein (ADF), thyrosin,
 CC parathymosin, mammary-derived growth inhibitor, galectin or rhodanase.
 CC The method is used to detect proteins, complexes of proteins, or parts of
 CC a larger complex, that bind to and mediate the transport of leaderless
 CC proteins, e.g. Na⁺/K⁺ ATPase which is an integral membrane protein
 CC responsible for transporting sodium and potassium ions across the cell
 CC membrane using ATP as the driving force. Transport molecules detected by
 CC the method are used in assays to identify inhibitors of the interaction
 CC with a leaderless protein.
 CC
 XX
 SQ Sequence 86 AA;
 XX
 Query Match 97.7%; Score 465; DB 21; Length 86;
 Best Local Similarity 97.6%; Pred. No. 1.3e-41;
 Matches 83; Conservative 0; Mismatches 0; Indels 2; Gaps 1;
 OY 1 EPVDPRLPEPKHPSGQPTACTNCCYKCCFHCQVCFITKA--ISYGRKKRRORRRPQG 58
 DB 2 EPVDPRLPEPKHPSGQPTACTNCCYKCCFHCQVCFITKALGISYGRKKRRORRRPQG 61
 OY 59 SQTHQVSLSKQPTSQSGRDPGPK 83
 DB 62 sqthqvslskqpsqsrqdpdpke 86
 DB
 RESULT 13
 AARI3379
 ID AARI3379 standard; Protein; 87 AA.
 XX
 AC AARI3379;
 XX
 DT 23-OCT-1991 (first entry)
 XX
 DE TAT protein.
 XX
 KM HIV; AIDS.
 XX

OS Synthetic.
 XX
 PN EP441582-A.
 XX
 PD 14-AUG-1991.
 PD
 XX 04-FEB-1991; 91EP-0300903.
 PF
 XX 09-FEB-1990; 90GB-0003010.
 PR
 XX (GLAX) GLAXO GROUP LTD.
 PA
 XX
 XX Dykes CW, Ernst JF, Hobden AN;
 PI
 XX WPI: 1991-240122/33.
 DR
 XX N-PSDB; AAQ13188.
 DR
 XX
 PT Gene expression system for yeast cells - with TAT protein
 PT mediated expression under the control of a HIV regulatory control
 PT sequence.
 PT
 XX
 PS Disclosure; Page 10; 26pp; English.
 XX
 CC The TAT protein here is encoded by the synthetic tat gene but is
 CC identical to the TAT protein found in HIV. The expression of the TAT
 CC protein in transformed yeast enables TAT inhibitory agents to be
 CC screened to obtain potential anti-viral agents esp. anti-HIV
 CC therapeutic agents.
 CC
 XX
 SQ Sequence 87 AA;
 XX
 Query Match 97.7%; Score 465; DB 12; Length 87;
 Best Local Similarity 97.6%; Pred. No. 1.3e-41;
 Matches 83; Conservative 0; Mismatches 0; Indels 2; Gaps 1;
 OY 1 EPVDPRLPEPKHPSGQPTACTNCCYKCCFHCQVCFITKA--ISYGRKKRRORRRPQG 58
 DB 2 EPVDPRLPEPKHPSGQPTACTNCCYKCCFHCQVCFITKALGISYGRKKRRORRRPQG 61
 OY 59 SQTHQVSLSKQPTSQSGRDPGPK 83
 DB 62 sqthqvslskqpsqsrqdpdpke 86
 DB
 RESULT 14
 AAY02350
 ID AAY02350 standard; Protein; 95 AA.
 XX
 AC AAY02350;
 XX
 DT 09-JUL-1999 (first entry)
 DT
 XX
 DE A representative HIV-1 Tat-His protein.
 XX
 KW HIV nef gene; fusion protein; HIV nef gene; Nef protein; Tat protein;
 KW vaccine; HIV infection; protein D.
 XX
 OS Synthetic.
 OS human immunodeficiency virus type 1.
 XX
 XX WO916884-A1.
 PN
 XX
 PD 08-APR-1999.
 PD
 XX
 PF 17-SEP-1998; 98WO-EP06040.
 PF
 XX 26-SEP-1997; 97GB-0020585.
 PR
 XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
 PA
 XX Bruck C, Godart SAG, Marchand M;
 PI
 XX

DR WPI: 1999-302282/25.
 DR N-PSDB: AAX35686.
 XX
 XX HIV Tat or Nef protein linked to a fusion partner
 XX
 XX Disclosure: Fig 2; 66pp; English.
 XX
 CC The present sequence represents a representative HIV-1 Tat-His protein.
 CC The protein is used in the creation of the fusion proteins of
 CC the invention, in conjunction with a fusion partner (e.g. protein D).
 CC The specification also describes fusion proteins comprising HIV-1 Nef
 CC protein. The fusion protein can be used in a vaccine to prevent HIV
 CC infection.
 CC
 XX
 SQ Sequence 95 AA;
 XX
 Query Match 97.7%; Score 465; DB 20; Length 95;
 Best Local Similarity 97.6%; Pred. No. 1.4e-41;
 Matches 83; Conservative 0; Mismatches 0; Indels 2; Gaps 1;
 QY 1 EPVDPRLPEPKHPSGQPTACTNCCYCKKCFHCQVCFITKA--ISYGRKKRRRRRPPQG 58
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 Db 2 EPVDPRLPEPKHPSGQPTACTNCCYCKKCFHCQVCFITKAISYGRKKRRRRRPPQG 61
 QY 59 SOTHQVSLSKOPTSOSRSGDPTGPKE 83
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 62 sqthqvsiskpptsqrgdptgpke 86
 RESULT 15
 AAG63232
 ID AAG63232 standard; protein; 95 AA.
 XX
 AC AAG63232;
 XX
 DT 01-OCT-2001 (first entry)
 XX
 DE Amino acid sequence of a His-tagged Tat protein of HIV.
 XX
 KW HIV; nef gene; tat gene; vaccine; gp120 gene; HIV viral load.
 XX
 OS Synthetic.
 OS Human immunodeficiency virus.
 XX
 PN WO200154719-A2.
 XX
 PD 02-AUG-2001.
 XX
 PF 29-JAN-2001; 2001WO-EP00944.
 XX
 PR 31-JAN-2000; 2000GB-0002200.
 PR 14-APR-2000; 2000GB-0009336.
 PR 06-JUN-2000; 2000GB-0013806.
 PR 28-JUN-2000; 2000WO-EP05998.
 XX
 PA (SMK) SMITHKLINE BEECHAM BIOLOGICALS.
 XX
 PI Voss G;
 XX
 DR WPI: 2001-476172/51.
 DR N-PSDB: AAH42876.
 XX
 XX New use of a human immunodeficiency virus (HIV) Tat, or Nef, or Nef
 PT linked to Tat (Nef-Tat) protein or polynucleotide and an HIV gp120
 PT protein or polynucleotide for the manufacture of a vaccine -
 XX
 PS Disclosure: Fig 1; 90pp; English.
 XX
 CC The present sequence represents a His-tagged Tat protein of HIV. The
 CC protein is expressed in the yeast *Pichia pastoris*, and is used to
 CC produce the vaccine in the invention. The specification describes
 CC the use of HIV Tat, HIV Nef, or Nef-Tat; and HIV gp120 in the

CC manufacture of a vaccine. The vaccine is used for the prophylactic or
 CC therapeutic immunization of humans against HIV. Tat, Nef or Nef-Tat act
 CC in synergy with gp120 in the treatment and prevention of HIV. The
 CC vaccine reduces the HIV viral load in HIV infected humans and results
 CC in a maintenance of CD4+ levels over those levels found in the absence
 CC of vaccination with HIV Tat, Nef or Nef-Tat and HIV gp120.
 CC
 XX
 SQ Sequence 95 AA;
 XX

Query Match 97.7%; Score 465; DB 22; Length 95;
 Best Local Similarity 97.6%; Pred. No. 1.4e-41;
 Matches 83; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 EPVDPRLPEPKHPSGQPTACTNCCYCKKCFHCQVCFITKA--ISYGRKKRRRRRPPQG 58
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 2 EPVDPRLPEPKHPSGQPTACTNCCYCKKCFHCQVCFITKAISYGRKKRRRRRPPQG 61
 QY 59 SOTHQVSLSKOPTSOSRSGDPTGPKE 83
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 Db 62 sqthqvsiskpptsqrgdptgpke 86

Search completed: January 10, 2002, 15:34:34
 Job time: 32 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 10, 2002, 15:34:02 ; Search time 12.59 Seconds

(without alignments)
148.354 Million cell updates/sec

Title: US-09-555-534-2

Perfect score: 476
Sequence: 1 EVDPRLEPMKHNPGSQPKTA.....VSLSKQRTSQSGRDPRTGPK 83

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
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3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfilest1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	465	97.7	86	1	US-08-450-257-1
2	465	97.7	86	1	US-08-450-246-1
3	465	97.7	86	1	US-08-450-098-1
4	465	97.7	86	1	US-08-451-233-1
5	465	97.7	86	1	US-08-450-236-1
6	465	97.7	86	3	US-07-808-452-1
7	465	97.7	86	3	US-09-030-613-19
8	465	97.7	86	4	US-09-124-800-6
9	465	97.7	86	4	US-09-451-905-19
10	465	97.7	86	5	PCT-US92-10770-1
11	465	97.7	86	5	PCT-US95-06077-2
12	449	94.3	86	2	US-08-505-210-1
13	449	94.3	86	4	US-09-099-333-1
14	434	91.2	82	1	US-08-053-079A-15
15	388	81.5	72	3	US-09-030-613-17
16	388	81.5	72	4	US-09-451-905-17
17	364	76.5	72	4	US-08-893-853-1
18	364	76.5	72	4	US-09-113-921-1
19	339	71.2	312	1	US-08-094-128A-27
20	339	71.2	312	1	US-08-455-674-27
21	339	71.2	312	1	US-08-455-992-27
22	339	71.2	312	1	US-08-455-972-27
23	339	71.2	312	5	PCT-US92-00652-27
24	331	69.5	72	1	US-07-910-867B-2
25	310	65.1	72	1	US-07-910-867B-5
26	304	63.9	72	1	US-07-910-867B-3
27	290	60.9	72	1	US-07-910-867B-1

28	256	53.8	56	1	US-08-450-257-7	Sequence 7, App11
29	256	53.8	56	1	US-08-450-246-7	Sequence 7, App11
30	256	53.8	56	1	US-08-450-098-7	Sequence 7, App11
31	256	53.8	56	1	US-08-451-233-7	Sequence 7, App11
32	256	53.8	56	1	US-08-450-236-7	Sequence 7, App11
33	195	41.0	37	1	US-07-724-500B-22	Sequence 22, App1
34	176	37.0	106	6	5204258-4	Patent No. 5204258
35	166.5	35.0	157	1	US-08-450-257-60	Sequence 60, App1
36	166.5	35.0	157	1	US-08-450-246-60	Sequence 60, App1
37	166.5	35.0	157	1	US-08-450-098-60	Sequence 60, App1
38	166.5	35.0	157	1	US-08-451-233-60	Sequence 60, App1
39	166.5	35.0	157	1	US-08-450-236-60	Sequence 60, App1
40	166	34.9	36	1	US-08-450-257-2	Sequence 2, App11
41	166	34.9	36	1	US-08-450-246-2	Sequence 2, App11
42	166	34.9	36	1	US-08-450-098-2	Sequence 2, App11
43	166	34.9	36	1	US-08-451-233-2	Sequence 2, App11
44	166	34.9	36	1	US-08-450-236-2	Sequence 2, App11
45	159	33.4	36	5	PCT-US95-06077-15	Sequence 15, App1

ALIGNMENTS

RESULT 1
US-08-450-257-1
; Sequence 1, Application US/08450257
; Patent No. 5652122
; GENERAL INFORMATION:
; APPLICANT: FRANKEL, Alan
; APPLICANT: PABO, Carl
; APPLICANT: BARSODI, James G.
; APPLICANT: FAMELL, Stephen E.
; APPLICANT: PEPINSKY, R. B.
; TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,257
; FILING DATE: 25-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/235,403
; FILING DATE: 28-APR-1994
; APPLICATION NUMBER: US 07/934,375
; FILING DATE: 21-AUG-1992
; APPLICATION NUMBER: US 07/098,766
; FILING DATE: 28-JUL-1993
; APPLICATION NUMBER: PCT/US93/07833
; FILING DATE: 19-AUG-1993
; APPLICATION NUMBER: US 07/454,450
; FILING DATE: 21-DEC-1989
; APPLICATION NUMBER: US 07/636,662
; FILING DATE: 02-JAN-1991
; APPLICATION NUMBER: US 08/158,015
; FILING DATE: 24-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James F.
; REGISTRATION/DOCKET NUMBER: 27,794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090

TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 86 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: human immunodeficiency virus
STRAIN: type 1
US-08-450-257-1

Query Match 97.7%; Score 465; DB 1; Length 86;
Best Local Similarity 97.6%; Pred. No. 6,4e-45;
Matches 83; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 EVDPRLPEPMKHPGSPKACTNCTCKKCFHCQVCFITKA--ISYGRKKRRRRRPPQG 58
DB 2 EVDPRLPEPMKHPGSPKACTNCTCKKCFHCQVCFITKALGISYGRKKRRRRRPPQG 61
QY 59 SOTHQVSLSKOPTSQSRGDPGTGPKE 83
DB 62 SOTHQVSLSKOPTSQSRGDPGTGPKE 86

RESULT 2
US-08-450-246-1
Sequence 1, Application US/08450246
Patent No. 5670617
GENERAL INFORMATION:
APPLICANT: FRANKEL, Alan
APPLICANT: PABO, Carl
APPLICANT: BARSOM, James G.
APPLICANT: FAMELL, Stephen E.
APPLICANT: PEPINSKY, R. B.
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,246
FILING DATE: 25-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/235,403
FILING DATE: 28-APR-1994
APPLICATION NUMBER: US 07/934,375
FILING DATE: 21-AUG-1992
APPLICATION NUMBER: US 07/098,766
FILING DATE: 28-JUL-1993
APPLICATION NUMBER: PCT/US93/07833
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 21-DEC-1989
APPLICATION NUMBER: US 07/636,662
FILING DATE: 02-JAN-1991
APPLICATION NUMBER: US 08/158,015
FILING DATE: 24-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B170 CIP 2

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 86 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: human immunodeficiency virus
STRAIN: type 1
US-08-450-246-1

Query Match 97.7%; Score 465; DB 1; Length 86;
Best Local Similarity 97.6%; Pred. No. 6,4e-45;
Matches 83; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 EVDPRLPEPMKHPGSPKACTNCTCKKCFHCQVCFITKA--ISYGRKKRRRRRPPQG 58
DB 2 EVDPRLPEPMKHPGSPKACTNCTCKKCFHCQVCFITKALGISYGRKKRRRRRPPQG 61
QY 59 SOTHQVSLSKOPTSQSRGDPGTGPKE 83
DB 62 SOTHQVSLSKOPTSQSRGDPGTGPKE 86

RESULT 3
US-08-450-098-1
Sequence 1, Application US/08450098
Patent No. 5674980
GENERAL INFORMATION:
APPLICANT: FRANKEL, Alan
APPLICANT: PABO, Carl
APPLICANT: BARSOM, James G.
APPLICANT: FAMELL, Stephen E.
APPLICANT: PEPINSKY, R. B.
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,098
FILING DATE: 25-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/235,403
FILING DATE: 28-APR-1994
APPLICATION NUMBER: US 07/934,375
FILING DATE: 21-AUG-1992
APPLICATION NUMBER: US 07/098,766
FILING DATE: 28-JUL-1993
APPLICATION NUMBER: PCT/US93/07833
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 21-DEC-1989
APPLICATION NUMBER: US 07/636,662
FILING DATE: 02-JAN-1991
APPLICATION NUMBER: US 08/158,015
FILING DATE: 24-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B170 CIP 2

NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B170 CIP 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 86 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORGANISM: human immunodeficiency virus
STRAIN: type 1
US-08-450-098-1

Query Match 97.7%; Score 465; DB 1; Length 86;
Best Local Similarity 97.6%; Pred. No. 6,4e-45;
Matches 83; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

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|||||
DB 2 EPVDPRLPMKHPGSOPTACTNCYCKKCCPHCOVCFITKALGISYGRKKRRRRRPPQG 61

OY 59 SOTHQVSLSKOPTSQSRDPTGPKE 83
|||||
DB 62 SOTHQVSLSKOPTSQSRDPTGPKE 86

RESULT 4

US-08-451-233-1

; Sequence 1, Application US/08451233
; Patent No. 5747641
; GENERAL INFORMATION:
; APPLICANT: FRANKEL, Alan
; APPLICANT: PABO, Carl
; APPLICANT: BARSOUM, James G.
; APPLICANT: FAWELL, Stephen E.
; APPLICANT: PEPINSKY, R. B.
; TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/451,233
; FILING DATE: 25-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/235,403
; FILING DATE: 28-APR-1994
; APPLICATION NUMBER: US 07/934,375
; FILING DATE: 21-AUG-1992
; APPLICATION NUMBER: US 07/098,766
; FILING DATE: 28-JUL-1993
; APPLICATION NUMBER: PCT/US93/07833
; FILING DATE: 19-AUG-1993
; APPLICATION NUMBER: US 07/454,450
; FILING DATE: 21-DEC-1989
; APPLICATION NUMBER: US 07/636,662
; FILING DATE: 02-JAN-1991

APPLICATION NUMBER: US 08/158,015
FILING DATE: 24-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B170 CIP 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 86 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORGANISM: human immunodeficiency virus
STRAIN: type 1
US-08-451-233-1

Query Match 97.7%; Score 465; DB 1; Length 86;
Best Local Similarity 97.6%; Pred. No. 6,4e-45;
Matches 83; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

OY 1 EPVDPRLPMKHPGSOPTACTNCYCKKCCPHCOVCFITKA--ISYGRKKRRRRRPPQG 58
|||||
DB 2 EPVDPRLPMKHPGSOPTACTNCYCKKCCPHCOVCFITKALGISYGRKKRRRRRPPQG 61

OY 59 SOTHQVSLSKOPTSQSRDPTGPKE 83
|||||
DB 62 SOTHQVSLSKOPTSQSRDPTGPKE 86

RESULT 5

US-08-450-236-1

; Sequence 1, Application US/08450236
; Patent No. 5804604
; GENERAL INFORMATION:
; APPLICANT: FRANKEL, Alan
; APPLICANT: PABO, Carl
; APPLICANT: BARSOUM, James G.
; APPLICANT: FAWELL, Stephen E.
; APPLICANT: PEPINSKY, R. B.
; TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,236
; FILING DATE: 25-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/235,403
; FILING DATE: 28-APR-1994
; APPLICATION NUMBER: US 07/934,375
; FILING DATE: 21-AUG-1992
; APPLICATION NUMBER: US 07/098,766
; FILING DATE: 28-JUL-1993
; APPLICATION NUMBER: PCT/US93/07833
; FILING DATE: 19-AUG-1993
; APPLICATION NUMBER: US 07/454,450

FILED DATE: 21-DEC-1989
APPLICATION NUMBER: US 07/636,662
FILING DATE: 02-JAN-1991
APPLICATION NUMBER: US 08/158,015
FILING DATE: 24-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B170 CIP 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 86 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: human immunodeficiency virus
STRAIN: type 1
US-08-450-236-1

Query Match 97.7%; Score 465; DB 1; Length 86;
Best Local Similarity 97.6%; Pred. No. 6.4e-45;
Matches 83; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 EPVDPRLPEPMKHGSGOPTACTNCYCKKCCFHQVCFTTKA--ISYGRKKRRRRRRPPQG 58
|||||
DB 2 EPVDPRLPEPMKHGSGOPTACTNCYCKKCCFHQVCFTTKALGISYGRKKRRRRRRPPQG 61
|||||
QY 59 SOTHQVSLSKOPTSOSRGPDPGPK 83
|||||
DB 62 SOTHQVSLSKOPTSOSRGPDPGPK 86
|||||

RESULT 6
US-07-808-452-1
Sequence 1, Application US/07808452
Patent No. 6063612
GENERAL INFORMATION:
APPLICANT: Jayasena, Sumedha D.
APPLICANT: Johnston, Brian H.
TITLE OF INVENTION: Antiviral Reagents Based on
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/808,452
FILING DATE: 19911213
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8255-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 86 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: the sequence of the TAR protein of
INDIVIDUAL ISOLATE: HIV-1
US-07-808-452-1

Query Match 97.7%; Score 465; DB 3; Length 86;
Best Local Similarity 97.6%; Pred. No. 6.4e-45;
Matches 83; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 EPVDPRLPEPMKHGSGOPTACTNCYCKKCCFHQVCFTTKA--ISYGRKKRRRRRRPPQG 58
|||||
DB 2 EPVDPRLPEPMKHGSGOPTACTNCYCKKCCFHQVCFTTKALGISYGRKKRRRRRRPPQG 61
|||||
QY 59 SOTHQVSLSKOPTSOSRGPDPGPK 83
|||||
DB 62 SOTHQVSLSKOPTSOSRGPDPGPK 86
|||||

RESULT 7
US-09-030-613-19
Sequence 19, Application US/09030613
Patent No. 6083706
GENERAL INFORMATION:
APPLICANT: Florjencic, Robert Z.
APPLICANT: Baird, J. Andrew
TITLE OF INVENTION: INHIBITORS OF LEADERLESS PROTEIN EXPORT
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,613
FILING DATE: 25-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: No. 6083706tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 760100.418C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 86 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-030-613-19

Query Match 97.7%; Score 465; DB 3; Length 86;
Best Local Similarity 97.6%; Pred. No. 6.4e-45;
Matches 83; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 EPVDPRLPEPMKHGSGOPTACTNCYCKKCCFHQVCFTTKA--ISYGRKKRRRRRRPPQG 58
|||||
DB 2 EPVDPRLPEPMKHGSGOPTACTNCYCKKCCFHQVCFTTKALGISYGRKKRRRRRRPPQG 61
|||||

QY 59 SQTHOVSLSKOPTSOSRGDPTGPKE 83
 Db 62 SQTHOVSLSKOPTSOSRGDPTGPKE 86

RESULT 8

US-09-124-900-6
 ; Sequence 6, Application US/09124900
 ; Patent No. 6268484
 ; GENERAL INFORMATION:
 ; APPLICANT: KATINGER, Hermann
 ; APPLICANT: BUCHACHER, Andrea
 ; APPLICANT: ERNST, Wolfgang
 ; APPLICANT: BALLAUN, Claudia
 ; APPLICANT: PURTSCHER, Martin
 ; APPLICANT: TRKOJA, Alexandra
 ; APPLICANT: PREDL, Renate
 ; APPLICANT: SCHWATZ, Christine
 ; APPLICANT: KLIMA, Annelies
 ; APPLICANT: STEINDL, Franz
 ; APPLICANT: MUSTER, Thomas
 ; TITLE OF INVENTION: HIV-Vaccines
 ; FILE REFERENCE: 1939-112P
 ; CURRENT APPLICATION NUMBER: US/09/124,900
 ; PRIOR FILING DATE: 1998-07-30
 ; PRIOR APPLICATION NUMBER: PCT/EP95/01481
 ; PRIOR FILING DATE: 1995-04-19
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: Patentin version 3.0
 ; SEQ ID NO 6
 ; LENGTH: 86
 ; TYPE: PR1
 ; ORGANISM: Human immunodeficiency virus type 1
 US-09-124-900-6

Query Match 97.7%; Score 465; DB 4; Length 86;
 Best Local Similarity 97.6%; Pred. No. 6,4e-45;
 Matches 83; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 EPVDPRLPEPMKHPGSOPTACTNCTCYKCCFHCQVCFITKA--ISYGRKKRRQRRRPPG 58
 Db 2 EPVDPRLPEPMKHPGSOPTACTNCTCYKCCFHCQVCFITKALGISYGRKKRRQRRRPPG 61
 QY 59 SQTHOVSLSKOPTSOSRGDPTGPKE 83
 Db 62 SQTHOVSLSKOPTSOSRGDPTGPKE 86

RESULT 9

US-09-451-905-19
 ; Sequence 19, Application US/09451905
 ; Patent No. 6306613
 ; GENERAL INFORMATION:
 ; APPLICANT: Robert Z. Florjancic
 ; APPLICANT: Andrew Baird
 ; APPLICANT: Dale E. Wainock
 ; TITLE OF INVENTION: MODULATORS OF LEADERLESS PROTEIN EXPORT
 ; FILE REFERENCE: 200124.402C4
 ; CURRENT APPLICATION NUMBER: US/09/451,905
 ; CURRENT FILING DATE: 1999-12-01
 ; NUMBER OF SEQ ID NOS: 48
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 19
 ; LENGTH: 86
 ; TYPE: PR1
 ; ORGANISM: Homo sapien
 US-09-451-905-19

Query Match 97.7%; Score 465; DB 4; Length 86;

Best Local Similarity 97.6%; Pred. No. 6,4e-45;
 Matches 83; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 EPVDPRLPEPMKHPGSOPTACTNCTCYKCCFHCQVCFITKA--ISYGRKKRRQRRRPPG 58
 Db 2 EPVDPRLPEPMKHPGSOPTACTNCTCYKCCFHCQVCFITKALGISYGRKKRRQRRRPPG 61
 QY 59 SQTHOVSLSKOPTSOSRGDPTGPKE 83
 Db 62 SQTHOVSLSKOPTSOSRGDPTGPKE 86

RESULT 10

PCT-US92-10770-1
 ; Sequence 1, Application PC/TUS9210770
 ; GENERAL INFORMATION:
 ; APPLICANT: Jayasena, Sumedha D.
 ; APPLICANT: Johnston, Brian H.
 ; TITLE OF INVENTION: Antiviral Reagents Based on
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Sri International
 ; STREET: 333 Ravenswood Avenue
 ; CITY: Menlo Park
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94025
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: IBM PC compatible
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US92/10770
 ; FILING DATE: 19921211
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/808,452
 ; FILING DATE: 13-DEC-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fadian, Gary R.
 ; REGISTRATION NUMBER: 33,875
 ; REFERENCE/DOCKET NUMBER: P-2962
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 859-4550
 ; TELEFAX: (415) 859-3880
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 86 amino acids
 ; TYPE: AMINO ACID
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; INDIVIDUAL ISOLATE: the sequence of the Tat protein of
 ; INDIVIDUAL ISOLATE: HIV-1
 ; PCT-US92-10770-1

Query Match 97.7%; Score 465; DB 5; Length 86;
 Best Local Similarity 97.6%; Pred. No. 6,4e-45;
 Matches 83; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 EPVDPRLPEPMKHPGSOPTACTNCTCYKCCFHCQVCFITKA--ISYGRKKRRQRRRPPG 58
 Db 2 EPVDPRLPEPMKHPGSOPTACTNCTCYKCCFHCQVCFITKALGISYGRKKRRQRRRPPG 61
 QY 59 SQTHOVSLSKOPTSOSRGDPTGPKE 83
 Db 62 SQTHOVSLSKOPTSOSRGDPTGPKE 86

RESULT 11
PCT-US95-06077-2
Sequence 2, Application PC/TUS9506077
GENERAL INFORMATION:
APPLICANT: Immunobiology Research, Institute Inc.
TITLE OF INVENTION: Vaccine Interdiction of Extracellular
TITLE OF INVENTION: Transactivating Proteins of Human Immunodeficiency Virus
TITLE OF INVENTION: and Other Chronically Infecting Viruses Employing Similar
TITLE OF INVENTION: Interellular Transactivating Strategies
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06077
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/247,991
FILING DATE: 23-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 86 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-06077-2

Query Match 97.7%; Score 465; DB 5; Length 86;
Best Local Similarity 97.6%; Pred. No. 6.4e-45;
Matches 83; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 EPVDPRLPEWKHPGSPQPTACTNCYCKKCFHCQVCFITKA--ISYGRKKRRQRRPPG 58
DB 2 EPVDPRLPEWKHPGSPQPTACTNCYCKKCFHCQVCFITKALGISYGRKKRRQRRPPG 61

QY 59 SOTHQVLSKOPTSQSRGDPGPKE 83
DB 62 SOTHQVLSKOPTSQSRGDPGPKE 86

RESULT 12
US-08-505-210-1
Sequence 1, Application US/08505210
Patent No. 5981258
GENERAL INFORMATION:
APPLICANT: MEHTALI, Majid
APPLICANT: GUSS, Tanja
TITLE OF INVENTION: COMPOSITION OF TRANS-DOMINANT VARIANTS
TITLE OF INVENTION: OF VIRAL PROTEINS FOR OBTAINING AN ANTIVIRAL EFFECT
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
STREET: 1737 King Street, Suite 500
CITY: Alexandria

STATE: Virginia
COUNTRY: United States
ZIP: 22314-2756
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/505,210
FILING DATE: 14-AUG-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,248
FILING DATE: 21-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR94/01457
FILING DATE: 13-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Dadio, Susan M.
REGISTRATION NUMBER: 40,373
REFERENCE/DOCKET NUMBER: 017753-066
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 86 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Human Immunodeficiency virus type 1
STRAIN: Lai
INDIVIDUAL ISOLATE: sequence of the TAT protein of HIV-1
US-08-505-210-1

Query Match 94.3%; Score 449; DB 2; Length 86;
Best Local Similarity 94.1%; Pred. No. 3.9e-43;
Matches 80; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 1 EPVDPRLPEWKHPGSPQPTACTNCYCKKCFHCQVCFITKA--ISYGRKKRRQRRPPG 58
DB 2 EPVDPRLPEWKHPGSPQPTACTNCYCKKCFHCQVCFITKALGISYGRKKRRQRRPPG 61

QY 59 SOTHQVLSKOPTSQSRGDPGPKE 83
DB 62 SOTHQVLSKOPTSQSRGDPGPKE 86

RESULT 13
US-09-099-333-1
Sequence 1, Application US/09099333A
Patent No. 6228369
GENERAL INFORMATION:
APPLICANT: MEHTALI, Majid
APPLICANT: GUSS, Tanja
TITLE OF INVENTION: COMPOSITION OF TRANS-DOMINANT VARIANTS OF VIRAL
TITLE OF INVENTION: PROTEINS FOR OBTAINING AN ANTI-VIRAL EFFECT
FILE REFERENCE: 017753-091
CURRENT APPLICATION NUMBER: US/09/099,333A
CURRENT FILING DATE: 1998-06-18
EARLIER APPLICATION NUMBER: FR 93 14914
EARLIER FILING DATE: 1993-12-13
EARLIER APPLICATION NUMBER: US 08/215,248
EARLIER FILING DATE: 1994-03-21
EARLIER APPLICATION NUMBER: US 08/505,210
EARLIER FILING DATE: 1995-08-14
NUMBER OF SEQ ID NOS: 7

SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 1
LENGTH: 86
TYPE: PR
ORGANISM: Human immunodeficiency virus type 1
US-09-099-333-1

Query Match 94.3%; Score 449; DB 4; Length 86;
Best Local Similarity 94.1%; Pred. No. 3.9e-43;
Matches 80; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 1 EPVDPRLPEPKHSGQPKTACTNCYCKCCFHCQVCFTKA--ISYGRKKRRQRRRPPG 58
|||||
DB 2 EPVDPRLPEPKHSGQPKTACTNCYCKCCFHCQVCFTKALGISYGRKKRRQRRRPPG 61
|||||
QY 59 SOTHQVSLSKOPTSOSRGDPTGPK 83
|||||
DB 62 SOTHQVSLSKOPTSOSRGDPTGPK 86

RESULT 14
US-08-053-079A-15
Sequence 15, Application US/08053079A
Patent No. 5606026
GENERAL INFORMATION:
APPLICANT: Rodman
TITLE OF INVENTION: Natural Human Igm Antibodies
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby
STREET: 805 Third Ave.
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,079A
FILING DATE: 26-APR-1993
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Robinson, Joseph, R.
REGISTRATION NUMBER: 33,448
REFERENCE/DOCKET NUMBER: 4436/160600S4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)527-7700
TELEFAX: (212)753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 82
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-053-079A-15

Query Match 91.2%; Score 434; DB 1; Length 82;
Best Local Similarity 96.3%; Pred. No. 1.7e-41;
Matches 78; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 1 EPVDPRLPEPKHSGQPKTACTNCYCKCCFHCQVCFTKA--ISYGRKKRRQRRRPPG 58
|||||
DB 2 EPVDPRLPEPKHSGQPKTACTNCYCKCCFHCQVCFTKALGISYGRKKRRQRRRPPG 61
|||||
QY 59 SOTHQVSLSKOPTSOSRGDPT 79
|||||
DB 62 SOTHQVSLSKOPTSOSRGDPT 82

RESULT 15
US-09-030-613-17
Sequence 17, Application US/09030613
Patent No. 6083706
GENERAL INFORMATION:
APPLICANT: Florkiewicz, Robert Z.
APPLICANT: Baird, J. Andrew
TITLE OF INVENTION: INHIBITORS OF LEADERLESS PROTEIN EXPORT
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,613
FILING DATE: 25-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6083706tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 760100.418C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 72 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-030-613-17

Query Match 81.5%; Score 388; DB 3; Length 72;
Best Local Similarity 97.2%; Pred. No. 1.9e-36;
Matches 69; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 EPVDPRLPEPKHSGQPKTACTNCYCKCCFHCQVCFTKA--ISYGRKKRRQRRRPPG 58
|||||
DB 2 EPVDPRLPEPKHSGQPKTACTNCYCKCCFHCQVCFTKALGISYGRKKRRQRRRPPG 61
|||||
QY 59 SOTHQVSLSKO 69
|||||
DB 62 SOTHQVSLSKO 72

Search completed: January 10, 2002, 15:35:15
Job time: 73 sec

Thu Jan 10 15:38:03 2002

us-09-555-534-2.rail

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OM protein - protein search, using sw model

Run on: January 10, 2002, 15:34:02 ; Search time 14.89 Seconds

(without alignments)
424.613 Million cell updates/sec

Title: US-09-555-534-2

Perfect score: 476
Sequence: 1 EPVDPRLPEPKHPGSGPRTA.....VSLSKOPTSOSRGDPGPKE 83

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR_68:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	465	97.7	86	2	S33982 trans-activating t
2	457	96.0	95	1	TNLIJ2 trans-activating t
3	449	94.3	86	2	A25700 trans-activating t
4	415	87.2	101	2	T09446 tat protein - huma
5	412	86.6	101	1	E44001 trans-activating t
6	390	81.9	86	2	JC5591 transactivator pro
7	387	81.3	86	2	S54381 tat protein - huma
8	384	80.7	86	1	TNLIJ2R trans-activating t
9	382	80.3	86	1	TNLIJ2D trans-activating t
10	374.5	78.7	87	2	T01655 tat protein - huma
11	344	72.3	72	1	TNLIJH4 trans-activating t
12	333	70.0	71	2	T09384 trans-activating t
13	297.5	62.5	100	1	TNLIJ1 trans-activating t
14	165.5	34.8	130	1	TNLIJG trans-activating t
15	160.5	33.7	130	1	TNLIJST trans-activating t
16	160.5	33.7	130	2	S53096 tat protein - huma
17	149	31.3	130	2	S12157 trans-activating t
18	148.5	31.2	130	1	TNLIJG2 trans-activating t
19	148	31.1	133	1	TNLIJCA trans-activating t
20	141.5	29.7	129	1	TNLIJ3 trans-activating t
21	139.5	29.3	106	1	TNLIJ2 trans-activating t
22	133.5	28.0	96	2	S08440 trans-activating t
23	126.5	25.6	132	2	T11564 tat protein - siml
24	122	25.6	100	1	TNLIJG4 trans-activating t
25	122	25.6	119	2	A46356 tat protein - siml
26	120	25.2	131	2	T11557 tat protein - siml
27	112.5	23.6	116	1	A48344 trans-activating t
28	106	22.3	73	2	S46349 trans-activating t
29	101.5	21.3	145	1	TNLIJBT trans-activating t

30	77.5	16.3	346	2	P96785 protein F10A5.26 l
31	76	16.0	171	1	BGB02 spermatid transiti
32	76	16.0	134	2	G84600 hypothetical prote
33	76	16.0	390	2	I51419 transcription fact
34	74	15.5	388	2	I51420 transcription fact
35	73.5	15.4	1477	2	T13797 tumor suppressor pr
36	72.5	15.2	222	2	E84560 hypothetical prote
37	72	15.1	137	1	BGP62 spermatid transiti
38	70.5	14.8	3942	2	T42730 Bassoon protein -
39	70	14.7	477	2	T23554 hypothetical prote
40	69.5	14.6	159	2	J00145 hypothetical 17.3k
41	69.5	14.6	1338	2	S64484 phosphatidylerine
42	69	14.5	322	2	T04595 hypothetical prote
43	69	14.5	3198	2	A43426 collagen alpha 2 f
44	68	14.3	944	1	S48821 probable membrane
45	67.5	14.2	895	2	T02597 Mutator-like trans

ALIGNMENTS

```
RESULT 1
S33982      trans-activating transcription regulator - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 06-Oct-1994 #sequence_revision 23-Feb-1996 #text_change 20-Sep-1999
C:Accession: S33982; S26385; S19864
R:Carlini, F.
Submitted to the EMBL Data Library, November 1991
A:Reference number: S33979
A:Accession: S33982
A:Molecule-type: DNA
A:Residues: 1-86 <CAR>
A:Cross-references: EMBL:115130; NID:g60192; PIDN:CAA77625.1; PID:g60196
R:Sidrovski, D.P.; Matsuyama, T.; Figgerio, E.; Chui, S.; Min, X.; Effle, H.; Summer
Nucleic Acids Res. 20, 5311-5320, 1992
A>Title: Random mutagenesis of the human immunodeficiency virus type-1 trans-activato
A:Reference number: S26385; MUID:93065196
A:Accession: S26385
A:Molecule type: nucleic acid
A:Residues: 1-86 <STD>
A:Cross-references: EMBL:X64650; NID:g60144; PIDN:CAA5921.1; PID:g60145
C:Genetics:
A:Gene: tat
A:Introns: 72/2
C:Superfamily: AIDS trans-activating transcription regulator
C:Keywords: AIDS; Immunodeficiency

Query Match      97.7%; Score 465; DB 2; Length 86;
Best local Similarity 97.6%; Pred. No. 1.2e-38;
Matches 83; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY      1 EPVDPRLPEPKHPGSGPRTACTNCCYCKCCFHCQVCETKA--ISYGRKKRRQRRPPQG 58
Db      |||||||
QY      2 EPVDPRLPEPKHPGSGPRTACTNCCYCKCCFHCQVCETKA--ISYGRKKRRQRRPPQG 61
Db      |||||||
QY      59 SOTHVSLSKOPTSOSRGDPGPKE 83
Db      |||||||
Db      62 SOTHVSLSKOPTSOSRGDPGPKE 86

RESULT 2
TNLIJ2      trans-activating transcription regulator - human immunodeficiency virus type 1 (isola
C:Species: human immunodeficiency virus type 1, HIV-1
A/Note: host Homo sapiens (man)
C>Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 02-Jul-1998
C:Accession: A04017
R:Araya, S.K.; Gallo, R.C.
Proc. Natl. Acad. Sci. U.S.A. 83, 2209-2213, 1986
A>Title: Three novel genes of human T-lymphotropic virus type III: Immune reactivity
A:Reference number: A94093; MUID:8617573
```

A:Accession: A04017
A:Molecule type: DNA
A:Residues: 1-95 <ARY>
C:Genetics:
A:Gene: tat
C:Superfamily: AIDS trans-activating transcription regulator
C:Keywords: AIDS; Immunodeficiency; transcription regulation

Query Match	96.0%;	Score 457;	DB 1;	Length 95;
Best Local Similarity	96.5%;	Pred. No. 7.8e-38;		
Matches	82;	Conservative	0;	Mismatches 1;
				Indels 2;
				Gaps 1;

```
QY      1 EPVDRRLRPMKHPGSGPRTACTNCCCKKCFHQCVCETKA--ISYGKKRRQRPRRPQG 58
        |||||
Db       11 EPPVDRRLRPMKHPGSGPRTACTNCCCKKCFHQCVCETITKALGISYGKKRRQRPRRAPQG 70
```

```
QY      59 SQTHQVSLSKQPTSQSRGDPGPKE 83
        |||||||
Db      71 SQTHQVSLSKQPTSQSRGDPGPKE 95
```

RESULT	3
A25700	

trans-activating transcription regulator - human immunodeficiency virus type 1 (isolator C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 28-Sep-1987 #sequence_revision 28-Sep-1987 #text_change 02-Jul-1998
C:Accession: A25700

A: Accession: A25700
 A: Reference number: A25700; MUID: 85244627
 Science 229, 74-77, 1985
 R, SOULIUSAI, U.; FALAIKA, R.; ROSEN, C. J. W.

C:Superfamily: AIDS trans-activating transcription regulator

Query Match	94.3%	Score 449;	DB 2;	Length 86;
Best Local Similarity	94.1%	Pred. NO. 4.4e-37;		
Matches 80; Conservative	0;	Mismatches 3;	Indels 2;	Gaps 1

```
QY      1 EVVDRLEPMWNGSQRPACTACINCYCKKCCFNQCVEITKA--ISYGKKRRQRKRPRQG    58  
        |||||  
        |||||  
        |||||  
        |||||  
        |||||  
        |||||  
        |||||  
        |||||  
        |||||  
        |||||  
Db       2 EVDRLERPMWNGSQRPACTACINCYCKKCFNQCVEITKALGISYGKKRQRKRPRQG    61
```

```
QY      59 SQTQVSLSKQPTSQSRGDPGPKE 83
        |||||
Db      62 SQTQVSLSKQPTSQPRGDPGPKE 86
```

RESULT 4
T09446

C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-Aug-1999
C:Accession: T09446

submitted to the EMBL Data Library, July 1996
A:Reference number: Z16673
A:Accession: T09446

A;Molecule type: DNA
A;Residues: 1-101 <PAN>
A;Cross-references: EMBL:U63632; NID:g1465777; PID:g1465783

A:Gene: tat
A;Introns: 72/2
C:Superfamily: AIDS trans-activating transcription regulator

Query Match	87.28;	Score 415;	DB 2;	Length 101;
Best Local Similarity	87.18;	Pred. No. 1e-33;		

Matches 74; Conservative 1; Mismatches 8; Indels 2; Gaps 1;

QY 1 EPVDRLEPMWHPGSPRTACTNCCCKKCEHCQVEITK - AISYGKKRRQRRRRPQG 58
||||| ||||||||| ||||||| ||||||||| ||
Db 2 EPVDSLEPMWHPGSPRTACTTCCYCKKCLHQCVEITKGLGISYGKKRRQRRRRAPQD 61

```
QY      59 SQTQVSLSKQPTSQSRGDPGPKE 83
        ||||| |||||:| |||||
Db      62 SQTQASLSKQPSQPRGDPGPKE 86
```

transactivating transcription regulator - human immunodeficiency virus type 1 (strains E44001

C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #r
N:Alternate names: tat protein

C:Accession: E44701
R.Li, Y.; Hui, H.; Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M.
J. Virol. 66, 6587-6600, 1992
A.Titles: Complete nucleotide sequence, genome organization and biological properties

A;Reference number: A44001; MUID:93021387
A;Accession: E44001
A;Molecule type: DNA
A;Residues: 1-101 <1TV>

A;Cross-references: GB:M93258
C;Genetics:
A;Gene: tat
A;Introns: 72/2

C;Superfamily: Aids trans-activating transcription regulator
C;Superfamily: Aids trans-activating transcription regulator
C;Keywords: AIDS; immunodeficiency; transcription regulation

Query match	85.0%	DR 1	Length 101
Best Local Similarity	85.9%	Pred. No. 2e-33	
Matches 73; Conservative	1;	Mismatches 9;	Indels 2; Gaps 1;

Qy 1 EPVDRLEPMKHPGSGPRTACINCYCKCCFHCQVEITK--AISYGRKKRRQRPRPG 58
||||| ||||| :||| ||||| ||||| | ||||| |||||
Db 2 EPPVDNLEPMKHPGSGPRTACNNCYCKCCFHCQVCTTKGLGISYGRKKRRQRPRPD 61

```

qy      59  SQTQVSLSKQPTSQSKGDPITGKE 83
        ||||| ||||| ||||| ||||| |
Db      62  SQTQSSLSKQPTSQLRGDPITGPT 86

```

transactivator protein - human immunodeficiency virus type 1

N:Alternate names: tat protein
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 17-Mar-1999
C:Accession: J05591

A:Title: A selection system to study protein-RNA interactions: Functional display of
 R:Reference number: JCS5591
 MjId: 97350867
 B:Biochem. Biophys. Res. Commun. 235, 806-811, 1997
 R:Hoilmann, S., Willbold, D.
 R:Hoilmann, S., Willbold, D.

A:Accession: J03351
A:Molecule type: protein
A:Residues: 1-86 <H02>
Comment: This protein is a key regulatory protein in the viral replication cycle and

F;22-31/Region: cysteine-rich

Query Match	81.9%;	Score 390;	DB 2;	Length 86;
Best Local Similarity	78.8%;	Pred. No. 2.4e-31;		
Matches 67; Conservative	5;	Mismatches 11;	Indels 2;	Gaps 1;

```
OY      1 EPVDRLEPRKHHPSDQETACTNOCYCKKCFHQQVFITK--AISYGKKRRRQRPPQG 58
        |||| :||| ||||||| :|||||:||||| ||||| ||||| ||||| ||||| |||||
Db      2 EKVDPNIIEPMNHGSDQETACNRCHCCKCCYHCQVCFITKTGLGISYGRKKRRQRPPSQG 61
```


A:Accession: F33943
 A:Molecule type: genomic RNA
 A:Residues: 1-130 <KUM>
 A:Cross-References: GB:M31113; NID:g1339798; PIDN:AAB01356.1; PID:g325753
 C:Genetics:
 A:Gene: tat
 A:Introns: 99/2
 C:Superfamily: AIDS trans-activating transcription regulator
 C:Keywords: transcription

Query Match 33.7%; Score 160.5; DB 1; Length 130;
 Best Local Similarity 40.6%; Pred. No. 7.2e-09;
 Matches 28; Conservative 14; Mismatches 26; Indels 1; Gaps 1;
 QY 16 OPTACTN-CYCKKCCFHQVCFITKAISYGRKKRRRRRPOGSQTHQVSLSKOPTSQS 74
 DB 45 QPLEACDNKCYCKKCCYHCQMCFLNKGIGIWTYERKGRRRRPFKTKAHSSASDKSISTR 104
 QY 75 RGDPTGPKE 83
 DB 105 TGNSSQPEKK 113

Search completed: January 10, 2002, 15:34:56
 Job time: 54 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 10, 2002, 15:34:02 ; Search time 11.72 Seconds

(without alignments)
259,657 Million cell updates/sec

Title: US-09-555-534-2

Perfect score: 476
Sequence: 1 EPVDPRLRPWKHNGSQPKTA.....VSLSKPTSGSRGDPFGPK 83

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	465	97.7	86	TAT_HV1B1	P04606 human immun
2	460	96.6	86	TAT_HV1P	P04607 human immun
3	457	96.0	86	TAT_HV1I2	P04326 human immun
4	449	94.3	86	TAT_HV1B2	P04610 human immun
5	439	92.2	102	TAT_HV1H	P05908 human immun
6	433	91.0	86	TAT_HV1H2	P04608 human immun
7	424	89.1	101	TAT_HV1J2	P20879 human immun
8	415	87.2	101	TAT_HV1C	P05906 human immun
9	414	87.0	101	TAT_HV1C4	P05907 human immun
10	413	86.8	101	TAT_HV1S1	P19553 human immun
11	412	86.6	101	TAT_HV1Y2	P35965 human immun
12	409	85.9	101	TAT_HV1M	P05905 human immun
13	409	85.9	101	TAT_HV1S3	P19552 human immun
14	397	83.4	101	TAT_HV1A2	P04614 human immun
15	397	83.4	101	TAT_HV1O	P20893 human immun
16	387	81.3	86	TAT_HV1I2	P12506 human immun
17	384	80.7	86	TAT_HV1Z6	P04609 human immun
18	382	80.3	86	TAT_HV1ND	P18804 human immun
19	374.5	78.7	87	TAT_HV1MA	P04613 human immun
20	371	77.9	99	TAT_HV1E	P04611 human immun
21	320	67.2	101	TAT_HV1U4	P24712 human immun
22	304	63.9	58	TAT_HV1B5	P04612 human immun
23	297.5	62.5	100	TAT_HV1C2	P17285 chimpanzee
24	165.5	34.8	130	TAT_HV2G1	P18044 human immun
25	160.5	33.7	130	TAT_HV2ST	P20880 human immun
26	159.5	33.5	130	TAT_HV2KR	P074124 human immun
27	150.5	31.6	130	TAT_HV1M	P05911 simian immun
28	149	31.3	130	TAT_HV2D1	P17759 human immun
29	148.5	31.2	130	TAT_HV2RO	P04605 human immun
30	148	31.1	133	TAT_HV2CA	P24109 human immun
31	147.5	31.0	130	TAT_HV2NE	P18098 human immun
32	145	30.5	130	TAT_HV2NE	P05909 human immun
33	139.5	29.3	106	TAT_HV1WL	P11263 simian immun

ALIGNMENTS

RESULT	ID	STANDARD	PRT	86 AA
1	TAT_HV1B1			
AC	P04606			
DT	13-AUG-1987 (Rel. 05, Created)			
DT	13-AUG-1987 (Rel. 05, Last sequence update)			
DT	20-AUG-2001 (Rel. 40, Last annotation update)			
DE	TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).			
GN	TAT.			
OS	Human immunodeficiency virus type 1 (BH10 isolate) (HIV-1), and			
OS	Human immunodeficiency virus type 1 (HX3 isolate) (HIV-1).			
OC	Viruses; Retroviridae; Retroviridae; Lentivirus.			
OX	NCBI_TaxID=11678, 11707;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-ISOLATE BH10;			
RX	MEDLINE=85111123; Pubmed=2578615;			
RA	Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R.,			
RA	Josephus S.F., Doran E.R., Ratajski J.A., Whitehorn E.A.,			
RA	Beaumeister K., Ivanoff L., Petelaw S.R., Jr., Pearson M.L.,			
RA	Lautenberger J.A., Papas T.S., Graybe J., Chang N.T., Gallo R.C.,			
RA	Wong-Staal F.;			
RT	"Complete nucleotide sequence of the AIDS virus, HTLV-III.";			
RL	Nature 313:277-284(1985).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-ISOLATE HXB3;			
RX	MEDLINE=85228248; Pubmed=2988795;			
RA	Crowl R., Ganguly K., Gordon M., Conroy R., Schaber M., Kramer R.,			
RA	Shaw G.M., Wong-Staal F., Reddy E.P.;			
RT	"HTLV-III env gene products synthesized in E. coli are recognized by			
RT	antibodies present in the sera of AIDS patients.";			
RL	Cell 41:979-986(1985).			
CC	-1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE			
CC	TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND			
CC	ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR			
CC	PROMOTER.			
CC	-1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).			
CC	-1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.			
CC	-1- MISCELLANEOUS: THE TWO ISOLATES TAR SEQUENCE ARE IDENTICAL.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	entities requires a license agreement (See http://www.1sb-sib.ch/announce/			
CC	or send an email to license@sib-sib.ch).			
CC	-----			
CC	EMBL: M14100; AAA44676.1; -			P12453 human immun
DR	EMBL: M15654; AAA44199.1; -			P05910 simian immun
DR	HIV: M15654; TATSH102.			P002838 simian immun
DR	HIV: M14100; TATSHXB3.			P15835 human immun
DR	InterPro: IP001831; HIV_Tat.			P19507 human immun
DR	Pfam: PF00539; Tat_1			P12513 simian immun
DR	PRINTS: PR00055; HIVTANDMAIN.			P27975 simian immun
				P05913 simian immun
				P27982 simian immun
				P12507 human immun
				P22384 simian immun
				P36340 simian immun

KW Transcription regulation; Activator; RNA-binding; Nuclear protein;
 KW AIDS.
 SO SEQUENCE 86 AA: 9784 MW: 4DD609415FAF9015 CRC64:

Query Match 97.7%; Score 465; DB 1; Length 86;
 Best Local Similarity 97.6%; Pred. No. 2e-41;
 Matches 83; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

OY 1 EVDPRLEPWKHPGSOPTACTNCCYCKCCFHCQVCFITKA--TSYGRKKRRRRRRPPQG 58
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 2 EVDPRLEPWKHPGSOPTACTNCCYCKCCFHCQVCFITKALGISYGRKKRRRRRRPPQG 61
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 OY 59 SOTHQVSLSKOPTSOSRGDPTGPKE 83
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 62 SOTHQVSLSKOPTSOSRGDPTGPKE 86

RESULT 2

TAT_HV1PV STANDARD; PRT; 86 AA.
 AC P04607;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).
 GN TAT.
 OS Human immunodeficiency virus type 1 (PV22 isolate) (HIV-1).
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 NC NCB1_TaxID=11700;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8511157; PubMed=2982104;
 RA Muesing M.A., Smith D.H., Cabradilla C.D., Benton C.V., Lasky L.A.,
 RA Capon D.J.;
 RT "Nucleic acid structure and expression of the human
 RT Aids/Lymphadenopathy retrovirus.";
 RL Nature 313:450-458(1985).
 CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
 CC -1- TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
 CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
 CC PROMOTER.
 CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
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 CC
 CC EMBL: K02083; AAB59870.1; -;
 CC EMBL: X01762; -; NOT_ANNOTATED_CDS.
 CC HIV: K02083; TATSPV22.
 CC InterPro: IPR001831; HIV_Tat.
 CC DR Pfam: PF00539; Tat; 1.
 CC DR PRINTS: PR00055; HIVTATDOMAIN.
 CC KW Transcription regulation; Activator; RNA-binding; Nuclear protein;
 KW AIDS.
 SO SEQUENCE 86 AA: 9794 MW: 4DD5C6415FAF9015 CRC64:

Query Match 96.6%; Score 460; DB 1; Length 86;
 Best Local Similarity 96.5%; Pred. No. 6.5e-41;
 Matches 82; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

OY 1 EVDPRLEPWKHPGSOPTACTNCCYCKCCFHCQVCFITKA--TSYGRKKRRRRRRPPQG 58
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 2 EVDPRLEPWKHPGSOPTACTNCCYCKCCFHCQVCFITKALGISYGRKKRRRRRRPPQG 61
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 OY 59 SOTHQVSLSKOPTSOSRGDPTGPKE 83

DB 62 SOTHQVSLSKOPTSOSRGDPTGPKE 86
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 3

TAT_HV112 STANDARD; PRT; 86 AA.
 AC P04326;
 DT 20-MAR-1987 (Rel. 04, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).
 GN TAT.
 OS Human immunodeficiency virus type 1 (clone 12) (HIV-1).
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 NC NCB1_TaxID=11679;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8617573; PubMed=3008154;
 RA Arya S.K., Gallo R.C.;
 RT "Three novel genes of human T-lymphotropic virus type III: Immune
 RT reactivity of their products with sera from acquired immune
 RT deficiency syndrome patients.";
 RT Proc. Natl. Acad. Sci. U.S.A. 83:2209-2213(1986).
 CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
 CC -1- TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
 CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
 CC PROMOTER.
 CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
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 CC
 CC EMBL: M11840; AAA4499.1; -;
 CC EMBL: P04017; TNLJ12.
 CC HIV: M11840; TATSPV12.
 CC InterPro: IPR001831; HIV_Tat.
 CC DR Pfam: PF00539; Tat; 1.
 CC DR PRINTS: PR00055; HIVTATDOMAIN.
 CC KW Transcription regulation; Activator; RNA-binding; Nuclear protein;
 KW AIDS.
 SO SEQUENCE 86 AA: 9758 MW: 4DD609414FBE9115 CRC64:

Query Match 96.0%; Score 457; DB 1; Length 86;
 Best Local Similarity 96.5%; Pred. No. 1.3e-40;
 Matches 82; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

OY 1 EVDPRLEPWKHPGSOPTACTNCCYCKCCFHCQVCFITKA--TSYGRKKRRRRRRPPQG 58
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 2 EVDPRLEPWKHPGSOPTACTNCCYCKCCFHCQVCFITKALGISYGRKKRRRRRRPPQG 61
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 OY 59 SOTHQVSLSKOPTSOSRGDPTGPKE 83
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 62 SOTHQVSLSKOPTSOSRGDPTGPKE 86

RESULT 4

TAT_HV1BR STANDARD; PRT; 86 AA.
 AC P04610;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).
 GN TAT.
 OS Human immunodeficiency virus type 1 (BRU isolate) (HIV-1).

```

OC  Viruses; Retroïd viruses; Retroviridae; Lentivirus.
OX  NCBI_TaxID=11686;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=85099333; PubMed=2981635;
RA  Wain-Hobson S.; Sonigo P.; Danos O.; Cole S.; Alizon M.;
RT  "Nucleotide sequence of the AIDS virus, LAV";
RL  Cell 40:9-17(1985).
RN  [2]
RP  SEQUENCE FROM N.A. (CLONE PNL4-3).
RA  Buckler C.E., Buckler-White A.J., Willey R.L., McCoy J.;
RL  Submitted (JUN-1988) to the EMBL/GenBank/DBJ databases.
CC  -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC  TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC  ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC  PROMOTER.
CC  -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC  -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
CC  -----
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL: K02013; AAB59745.1; -
DR  EMBL: M19921; AAA44985.1; -.
DR  HIV: K02013; TATSRU.
DR  HIV: M19921; TATSNL43.
DR  InterPro: IPR001831; HIV_Tat.
DR  Pfam: PF00539; Tat; 1.
DR  PRINTS: PR00055; HIVTATDOMAIN.
KM  Transcription regulation; Activator; RNA-binding; Nuclear protein;
KW  AIDS.
FT  VARIANT 24 24 T -> N (IN CLONE PNL4-3).
FT  VARIANT 39 39 T -> M (IN CLONE PNL4-3).
FT  VARIANT 58 61 PPOG -> AHON (IN CLONE PNL4-3).
FT  VARIANT 67 67 V -> A (IN CLONE PNL4-3).
FT  VARIANT 77 77 P -> S (IN CLONE PNL4-3).
SQ  SEQUENCE 86 AA; 9769 MW; 9B1BA913FAF8A14 CRC64;

Query Match 94.3%; Score 449; DB 1; Length 86;
Best Local Similarity 94.1%; Pred. No. 8.7e-40;
Matches 80; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

OY 1 EPVDPRLPEPKHSGOPKTACTNCYCKKCCFHCQVCFITK--ISYGRKKRRORRRPPOG 58
    |||||||
DB 2 EPVDPRLPEPKHSGOPKTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRORRRPPOG 61
    |||||||
OY 59 SOTHQVSLSKOPTSOSRGDPTGPK 83
    |||||||
DB 62 SOTHQVSLSKOPTSOSRGDPTGPK 86
    |||||||

RESULT 5
TAT_HV1RH STANDARD; PRT; 102 AA.
ID TAT_HV1RH
AC P05908;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).
GN TAT.
OS Human immunodeficiency virus type 1 (HF/HAT isolate) (HIV-1).
OC Viruses; Retroïd viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11701;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86218077; PubMed=2423250;
RA Starcich B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S.,

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RA Wolf H., Parks E.S., Parks W.P., Josephs S.F., Gallo R.C.,
RA Wong-Staal F.;
RT "Identification and characterization of conserved and variable
RT regions in the envelope gene of HTLV-III/LAV, the retrovirus of
RT AIDS.";
RL Cell 45:637-648(1986).
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M17451; TATSRF.
DR HIV: M17451; TATSRF.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat; 1.
DR PRINTS: PR00055; HIVTATDOMAIN.
KM Transcription regulation; Activator; RNA-binding; Nuclear protein;
KW AIDS.
SQ SEQUENCE 102 AA; 11538 MW; 3EACFB843C5195BD CRC64;

Query Match 92.2%; Score 439; DB 1; Length 102;
Best Local Similarity 90.6%; Pred. No. 1.1e-38;
Matches 77; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

OY 1 EPVDPRLPEPKHSGOPKTACTNCYCKKCCFHCQVCFITK--AISYGRKKRRORRRPPOG 58
    |||||||
DB 2 EPVDPRLPEPKHSGOPKTACTNCYCKKCCFHCQVCFITKGLISYGRKKRRORRRPPOG 61
    |||||||
OY 59 SOTHQVSLSKOPTSOSRGDPTGPK 83
    |||||||
DB 62 SOTHQVSLSKOPTSOSRGDPTGPK 86
    |||||||

RESULT 6
TAT_HV1H2 STANDARD; PRT; 86 AA.
ID TAT_HV1H2
AC P04608; O09778;
DT 13-AUG-1987 (Rel. 05, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).
GN TAT.
OS Human immunodeficiency virus type 1 (HXB2 isolate) (HIV-1).
OC Viruses; Retroïd viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11706;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8729196; PubMed=3040055;
RA Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S.,
RA Gallo R.C., Wong-Staal F.;
RT "Complete nucleotide sequences of functional clones of the AIDS
RT virus.";
RL AIDS Res. Hum. Retroviruses 3:57-69(1987).
RN [2]
RP REVISIONS.
RA Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S.,
RA Gallo R.C., Wong-Staal F.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.

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CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: K03455; AAB50256.1; -.
DR EMBL: AF033819; AAC82591.1; -.
DR HIV: K03455; TATSHXB2.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat; 1.
DR PRINTS: PR00055; HIVTATDOMAIN.
KW Transcription regulation; Activator; RNA-binding; Nuclear protein;
KW AIDS.
SQ SEQUENCE 86 AA: 9837 MW: 4DDC56D979769115 CRC64;

Query Match
Best Local Similarity 91.0%; Score 433; DB 1; Length 86;
Matches 78; Conservative 0; Mismatches 5; Indels 2; Gaps 1;

OY 1 EVDPRLEPMKHPGSGOPTACTNCYCKKCFHCQVCFITK--AISYGRKKRRRRRPPQG 58
DB 2 EVDPRLEPMKHPGSGOPTACTNCYCKKCFHCQVCFITKALGISYGRKKRRRRRPPQD 61
OY 59 SOTHQVSLSKOPTSOSRQDPTGPKE 83
DB 62 SOTHQVSLSKOPTSOSRQDPTGPKE 86

RESULT 7
TAT_HV1JR STANDARD: PRT; 101 AA.
AC P20879;
DR 01-FEB-1991 (Rel. 17, Created)
DR 01-FEB-1991 (Rel. 17, Last sequence update)
DR 20-AUG-2001 (Rel. 40, Last annotation update)
DE TAT PROTEIN (TRANSCRIPTIVATING REGULATORY PROTEIN).
GN TAT.
OS Human immunodeficiency virus type 1 (JRCSF isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11688;
RN [1]
RP SEQUENCE FROM N.A.
RA Koyanagi S., Chen I.S.Y.;
RL Submitted (DEC-1988) to the HIV data bank.
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
CC -----
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CC -----
DR EMBL: M38429; -. NOT_ANNOTATED_CDS.
DR HIV: M38429; TATSRCSF.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat; 1.
DR PRINTS: PR00055; HIVTATDOMAIN.
KW Transcription regulation; Activator; RNA-binding; Nuclear protein;
KW AIDS.

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SQ SEQUENCE 101 AA: 11508 MW: 3E6CBDBFF7F8D4FA CRC64;

Query Match
Best Local Similarity 89.1%; Score 424; DB 1; Length 101;
Matches 75; Conservative 1; Mismatches 7; Indels 2; Gaps 1;

OY 1 EVDPRLEPMKHPGSGOPTACTNCYCKKCFHCQVCFITK--AISYGRKKRRRRRPPQG 58
DB 2 EVDPRLEPMKHPGSGOPTACTNCYCKKCFHCQVCFITKALGISYGRKKRRRRRPPQD 61
OY 59 SOTHQVSLSKOPTSOSRQDPTGPKE 83
DB 62 SOTHQVSLSKOPTSOSRQDPTGPKE 86

RESULT 8
TAT_HV1SC STANDARD: PRT; 101 AA.
AC P05906;
DR 01-NOV-1988 (Rel. 09, Created)
DR 01-NOV-1988 (Rel. 09, Last sequence update)
DR 20-AUG-2001 (Rel. 40, Last annotation update)
DE TAT PROTEIN (TRANSCRIPTIVATING REGULATORY PROTEIN).
GN TAT.
OS Human immunodeficiency virus type 1 (SC isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11702;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=88219542; PubMed=3369091;
RA Gurgu C., Guo H.-G., Franchini G., Aldovini A., Collalti E.,
RA Farrell K., Wong-Staal F., Gallo R.C., Reitz M.S. Jr.;
RT "Envelope sequences of two new United States HIV-1 isolates.";
RL Virology 164:531-536(1988).
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
CC -1- MISCELLANEOUS: THE SC ISOLATE WAS TAKEN FROM AN ARC PATIENT IN
CC 1984 IN SOUTHERN CALIFORNIA.
CC -----
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CC -----
DR EMBL: M17450; AAA45060.1; -.
DR HIV: M17450; TATVSC.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat; 1.
DR PRINTS: PR00055; HIVTATDOMAIN.
KW Transcription regulation; Activator; RNA-binding; Nuclear protein;
KW AIDS.
SQ SEQUENCE 101 AA: 11426 MW: C9109B938D15788 CRC64;

Query Match
Best Local Similarity 87.2%; Score 415; DB 1; Length 101;
Matches 73; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

OY 1 EVDPRLEPMKHPGSGOPTACTNCYCKKCFHCQVCFITK--AISYGRKKRRRRRPPQG 58
DB 2 EVDPRLEPMKHPGSGOPAACTSCYCKKCFHCQVCFITKALGISYGRKKRRRRRAPD 61
OY 59 SOTHQVSLSKOPTSOSRQDPTGPKE 83
DB 62 SOTHQVSLSKOPTSOSRQDPTGPKE 86

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RESULT 9
TAT_HV1C4
ID TAT_HV1C4 STANDARD; PRT; 101 AA.
AC P05907;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE TAT PROTEIN (TRANSACTIVATING REGULATOR PROTEIN).
GN TAT.
OS Human immunodeficiency virus type 1 (CDC-451 isolate) (HIV-1).
OC Viruses; Retrovirdae; Lentiviruses.
OX NCBI_TaxID=11687;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87041461; PubMed=3490666;
RA Desai S.M., Kalyanaraman V.S., Casey J.M., Srinivasan A.,
RA Andersen P.R., Devare S.G.;
RT "Molecular cloning and primary nucleotide sequence analysis of a
RT distinct human immunodeficiency virus isolate reveal significant
RT divergence in its genomic sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:8380-8384(1986).
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
CC -----
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CC -----
DR EMBL: M13137; AAA44309.1; -.
DR PIR: B25523; TNJH4.
DR HIV: M13137; TATSCDC45.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat; 1.
DR PRINTS: PR00055; HIVTATDOMAIN.
KM Transcription regulation; Activator; RNA-binding; Nuclear protein;
KM AIDS.
SQ SEQUENCE 101 AA; 11594 MW; 817D915F3FB1C7FA CRC64;
```

```
OX NCBI_TaxID=11691;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90347835; PubMed=2384920;
RA Cheng-Mayer C., Quiroga M., Tung J.W., Dina D., Levy J.;
RT "Viral determinants of human immunodeficiency virus type 1 T-cell or
RT macrophage tropism, cytopathogenicity, and CD4 antigen modulation.";
RL J. Virol. 64:4390-4398(1990).
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
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CC -----
DR EMBL: M65024; AAA5069.1; -.
DR HIV: M38428; TATSEF162.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat; 1.
DR PRINTS: PR00055; HIVTATDOMAIN.
KM Transcription regulation; Activator; RNA-binding; Nuclear protein;
KM AIDS.
SQ SEQUENCE 101 AA; 11497 MW; 8CE2C48C2C63293C CRC64;
```

Query Match 86.8%; Score 413; DB 1; Length 101;
Best Local Similarity 85.9%; Pred. No. 5e-36;
Matches 73; Conservative 2; Mismatches 8; Indels 2; Gaps 1;

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QY 1 EPVDPRLPEPKHPSQPTACTNCYCKKCFHCVCFTTK--AISYGRKKRRORRRPPQG 58
    |||||
DB 2 EPVDPRLPEPKHPSQPTACTNCYCKKCFHCVCFTTGLGISYGRKKRRORRRAPPD 61
    |||||
QY 59 SQTHQVSLSKOPTSQSRGDPGPKE 83
    |||||
DB 62 SEVHQVSLPKOPASQSGDPGPKE 86
    |||||
```

RESULT 11
TAT_HV1Y2
ID TAT_HV1Y2 STANDARD; PRT; 101 AA.
AC P35965;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE TAT PROTEIN (TRANSACTIVATING REGULATOR PROTEIN).
GN TAT.
OS Human immunodeficiency virus type 1 (YU-2 isolate) (HIV-1).
OC Viruses; Retrovirdae; Lentiviruses.
OX NCBI_TaxID=36377;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93021387; PubMed=1404605;
RA Li Y., Hui H., Burgess C.J., Price R.W., Sharp P.M., Hahn B.H.,
RA Shaw G.M.;
RT "Complete nucleotide sequence, genome organization, and biological
RT properties of human immunodeficiency virus type 1 in vivo: evidence
RT for limited defectiveness and complementation.";
RL J. Virol. 66:6587-6600(1992).
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.

Db 62 S0NHQSLSKOPSSOPRBDPTGPK 86

RESULT 14

TAT_HV1A2 STANDARD: PRT: 101 AA.

AC P04614;

DT 13-AUG-1987 (Rel. 05, Created)

DT 13-AUG-1987 (Rel. 05, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).

TAT.

OS Human immunodeficiency virus type 1 (ARV2/SF2 isolate) (HIV-1).

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_Taxid=11685;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=85090453; Pubmed=2578227;

RA Sanchez-Pescador R., Power M.D., Barr P.J., Steimer K.S.,

Stempien M.M., Brown-Shimer S.L., Gee W.W., Renard A., Randolph A.,

Levy J.A., Dina D., Luciw P.A.;

"Nucleotide sequence and expression of an AIDS-associated retrovirus

(ARV-2)." ;

RL Science 227:484-492(1985).

CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE

CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND

CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR

CC PROMOTER.

CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.

CC -----

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CC -----

DR EMBL: K02007; AAB59879.1; -

DR HIV: K02007; TATSF2. HIV_Tat.

DR InterPro: IPR001831; HIV_Tat.

DR Pfam: PF00539; Tat; 1.

DR PRINTS: PR00055; HIVTATDOMAIN.

KW Transcription regulation; Activator; RNA-binding; Nuclear protein;

KW AIDS.

SO SEQUENCE 101 AA; 11557 MW; 1762370A3BD641FD CRC64;

Query Match 83.4%; Score 397; DB 1; Length 101;

Best Local Similarity 82.4%; Pred. No. 2,2e-34;

Matches 70; Conservative 1; Mismatches 12; Indels 2; Gaps 1;

OY 1 EPVDRLPEWKNPGSOPKTACTNCCYCKCFHCOVCFITK--AISYGRKKRRRRRRPQG 58

Db 2 EPVDRLPEWKNPGSOPKTACTNCCYCKCFHCOVCFITK--AISYGRKKRRRRRRPQG 61

OY 59 S0THQVSLSKOPSSOPRBDPTGPK 83

Db 62 S0THQVSLSKOPSSOPRBDPTGPK 86

RESULT 15

TAT_HV1OY STANDARD: PRT: 101 AA.

AC P20893;

DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).

TAT.

OS Human immunodeficiency virus type 1 (OVI isolate) (HIV-1).

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_Taxid=11699;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=90148544; Pubmed=2559749;

RA Huot T., Dazza M.C., Brun-Vezinet F., Roelants G.E., Main-Hobson S.;

"A highly defective HIV-1 strain isolated from a healthy Gabonese

individual presenting an atypical western blot." ;

RL AIDS 3:707-715(1989).

CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE

CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND

CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR

CC PROMOTER.

CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.

CC -1- MISCELLANEOUS: THE OVI ISOLATE WAS TAKEN FROM THE BLOOD OF A

CC HEALTHY GABONESE INDIVIDUAL.

CC -1- MISCELLANEOUS: THE SINGLE C->S SUBSTITUTION AT RESIDUE 22 OF THE

CC OVI TAT PROTEIN REDUCES IT INACTIVE, BUT MAY NOT ACCOUNT FOR THE

CC AVIRENCE OF THE VIRUS.

CC -----

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CC -----

DR EMBL: M26727; AAA83395.1; -

DR HIV: M26727; TATSOY1.

DR InterPro: IPR001831; HIV_Tat.

DR Pfam: PF00539; Tat; 1.

DR PRINTS: PR00055; HIVTATDOMAIN.

KW Transcription regulation; Activator; RNA-binding; Nuclear protein;

KW AIDS.

SO SEQUENCE 101 AA; 11561 MW; 83ACAC36C4C87AD CRC64;

Query Match 83.4%; Score 397; DB 1; Length 101;

Best Local Similarity 83.5%; Pred. No. 2,2e-34;

Matches 71; Conservative 2; Mismatches 10; Indels 2; Gaps 1;

OY 1 EPVDRLPEWKNPGSOPKTACTNCCYCKCFHCOVCFITK--AISYGRKKRRRRRRPQG 58

Db 2 EPVDRLPEWKNPGSOPKTACTNCCYCKCFHCOVCFITK--AISYGRKKRRRRRRPQG 61

OY 59 S0THQVSLSKOPSSOPRBDPTGPK 83

Db 62 S0THQVSLSKOPSSOPRBDPTGPK 86

Search completed: January 10, 2002, 15:36:01
Job time: 119 sec

Thu Jan 10 15:38:05 2002

us-09-555-534-2.rsp

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 10, 2002, 15:34:02 ; Search time 21.91 Seconds
(without alignments)
554.112 Million cell updates/sec

Title: US-09-555-534-2
Perfect score: 476
Sequence: 1 EVDPRLEPWKHPGSGPRTKA.....VLSKOPTSGSRGDPGPKE 83

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_17:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	437	91.8	86	12	Q74087 human immun
2	433	91.0	86	12	Q99BV4 human immun
3	432	90.8	101	12	Q92880 human immun
4	430	90.3	86	12	Q99BV5 human immun
5	429	90.1	86	12	Q57293 simian-huma
6	429	90.1	101	12	Q9DHA9 human immun
7	427	89.7	86	12	Q99BV6 human immun
8	427	89.7	86	12	Q99BV3 human immun
9	427	89.7	101	12	Q99BV7 human immun
10	426	89.5	86	12	Q99BV1 human immun
11	426	89.5	86	12	Q99BV0 human immun
12	426	89.5	101	12	Q9DH20 human immun
13	425	89.3	101	12	Q56318 simian-huma
14	425	89.3	101	12	Q92885 human immun
15	425	89.3	101	12	Q92899 human immun
16	424	89.1	101	12	Q92893 human immun
17	424	89.1	101	12	Q99BV8 human immun
18	423	88.9	101	12	Q9DQ29 human immun
19	420	88.2	101	12	Q04191 human immun

20	420	88.2	101	12	P90265 human immun
21	420	88.2	101	12	O11405 simian-huma
22	419	88.0	101	12	O40219 human immun
23	418	87.8	101	12	O74810 human immun
24	417	87.6	101	12	O80270 human immun
25	417	87.6	101	12	O77688 human immun
26	417	87.6	101	12	O93022 human immun
27	417	87.6	101	12	O9WJV2 human immun
28	416	87.4	101	12	Q99BV9 human immun
29	415	87.2	101	12	O75758 human immun
30	414.5	87.1	100	12	O73370 human immun
31	414	87.0	101	12	O72990 human immun
32	414	87.0	101	12	O92895 human immun
33	414	87.0	101	12	O92902 human immun
34	412	86.6	86	12	O906V3 human immun
35	412	86.6	101	12	O04192 human immun
36	412	86.6	101	12	O74747 human immun
37	412	86.6	101	12	O93199 human immun
38	412	86.6	101	12	O9WJV7 human immun
39	412	86.6	101	12	O9WJV9 human immun
40	412	86.6	101	12	O9W9E3 human immun
41	410	86.1	101	12	O72493 human immun
42	408	85.7	101	12	O71973 human immun
43	408	85.7	102	12	O91BN6 human immun
44	407	85.5	101	12	O89541 human immun
45	407	85.5	101	12	O9JAC4 human immun

ALIGNMENTS

RESULT	ID	PRELIMINARY	PRT	86 AA.
Q74087	Q74087			
AC	Q74087			
DT	01-NOV-1996 (TREMblrel. 01, Created)			
DT	01-NOV-1996 (TREMblrel. 01, Last sequence update)			
DT	01-JUN-2001 (TREMblrel. 17, Last annotation update)			
DE	TAT.			
GN	TAT.			
OS	Human immunodeficiency virus type 1.			
OC	Viruses; Retrovird viruses; Retroviridae; Lentivirus.			
OX	NCBI_TaxID=11676;			
ON	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=PM213;			
RA	Cloyd M.W., Moore B.E.;			
RT	"Spectrum of Biological Properties of Human Immunodeficiency Virus (HIV-1) Isolates."			
RL	Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=PM213;			
RA	Iwatani Y.;			
RL	Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: D86069; BAA13000.1; -			
DR	InterPro: IPR001831; HIV_Tat.			
DR	Pfam: PF00539; Tat.1			
DR	PRINTS: PR00055; HIVTRIDOMAIN.			
SO	SEQUENCE 86 AA; 9865 MW; 4DDC56CICE269115 CRC64;			
Query Match	Best Local Similarity	91.8%;	Score 437;	DB 12; Length 86;
Matches 79;	Conservative	0;	Mismatches 4;	Indels 2; Gaps 1;
QY	1 EVDPRLEPWKHPGSGPRTKA--ISYGRKKRRRRPPGG 58			
Db	2 EVDPRLEPWKHPGSGPRTKACNCKKCFHCQVCITRALGISYGRKKRRRRRAHNN 61			
QY	59 SOTHVSLSKOPTSGSRGDPGPKE 83			
Db	62 SOTHVSLSKOPTSGSRGDPGPKE 86			

```
RESULT 2
099BV4 ID 099BV4 PRELIMINARY; PRT; 86 AA.
AC 099BV4.
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE TAT PROTEIN.
GN TAT.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PI2.2;
RA Aldous M.C., Schwager M., Mok J.Y.Q., Yirell D.L., Leigh Brown A.J.,
RA Fiebel K.S.;
RT "The natural history of pediatric HIV infection suggests an
RT association between the specificity of the cytotoxic T cells and
RT clinical outcome.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF324449; AAK14291.1; -
SQ SEQUENCE 86 AA; 9842 MW; 60C7F0727C482F49 CRC64;

Query Match 91.0%; Score 433; DB 12; Length 86;
Best Local Similarity 90.6%; Pred. No. 1.8e-43;
Matches 77; Conservative 1; Mismatches 5; Indels 2; Gaps 1;

OY 1 EPVDRLEPMKHPGSOPTACTNCYCKKCCFHCQVCFTTK--AISYGRKKRRRRRPPQG 58
DB 2 EPVDRLEPMKHPGSOPTACTNCYCKKCCFHCQVCFTTKGIGISYGRKKRRRRRSPQS 61
OY 59 SOTHQVSLSKOPTSOSRDPPTGPK 83
DB 62 SOTHQVSLSKOPTSOPRDPPTGPK 86

RESULT 3
092880 ID 092880 PRELIMINARY; PRT; 101 AA.
AC 092880.
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE TAT PROTEIN.
GN TAT.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC200;
RA Oelrichs R.B., McPhee D.A., Deacon N.J.;
RT "Biological cloning and full-length sequence of two Australian HIV-1
RT primary clinical isolates with distinct cellular tropism and
RT cytopathicity.";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF042100; AAD03194.1; -
DR InterPro; IPR001831; HIV_Tat.
DR Pfam; PF00539; Tat; 1.
DR PRINTS; PR00055; HIVTATDOMAIN.
SQ SEQUENCE 101 AA; 11593 MW; A9F467BD68399235 CRC64;

Query Match 90.8%; Score 432; DB 12; Length 101;
Best Local Similarity 90.6%; Pred. No. 2.6e-43;
Matches 77; Conservative 1; Mismatches 5; Indels 2; Gaps 1;

OY 1 EPVDRLEPMKHPGSOPTACTNCYCKKCCFHCQVCFTTK--AISYGRKKRRRRRPPQG 58
|||||
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DB 2 EPVDRLEPMKHPGSOPTACTNCYCKKCCFHCQVCFTTKGIGISYGRKKRRRRRAPD 61
OY 59 SOTHQVSLSKOPTSOSRDPPTGPK 83
DB 62 SOTHQVSLSKOPTSOPRDPPTGPK 86

RESULT 4
099BV5 ID 099BV5 PRELIMINARY; PRT; 86 AA.
AC 099BV5.
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE TAT PROTEIN.
GN TAT.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PI2.1;
RA Aldous M.C., Schwager M., Mok J.Y.Q., Yirell D.L., Leigh Brown A.J.,
RA Fiebel K.S.;
RT "The natural history of pediatric HIV infection suggests an
RT association between the specificity of the cytotoxic T cells and
RT clinical outcome.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF324448; AAK14290.1; -
SQ SEQUENCE 86 AA; 9828 MW; C1C6E1727D928438 CRC64;

Query Match 90.3%; Score 430; DB 12; Length 86;
Best Local Similarity 89.4%; Pred. No. 4e-43;
Matches 76; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

OY 1 EPVDRLEPMKHPGSOPTACTNCYCKKCCFHCQVCFTTK--AISYGRKKRRRRRPPQG 58
DB 2 EPVDRLEPMKHPGSOPTACTNCYCKKCCFHCQVCFTTKGIGISYGRKKRRRRRSPQS 61
OY 59 SOTHQVSLSKOPTSOSRDPPTGPK 83
DB 62 SOTHQVSLSKOPTSOPRDPPTGPK 86

RESULT 5
057293 ID 057293 PRELIMINARY; PRT; 86 AA.
AC 057293.
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE TAT PROTEIN.
GN TAT.
OS Simian-Human immunodeficiency virus.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=57667;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SHIV-4, HXB2;
RA Cayabyab M., Karlsson G.B., Etemad-Moghadam B., Hofmann W.,
RA Haljoran M., Axelholm M.W., Letvin N.L., Sodroski J.G.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SHIV-4, HXB2;
RX MEDLINE=92309177; PubMed=1613662;
RA Li J., Lord C.I., Haseltine W., Letvin N.L., Sodroski J.;
RT "Infection of cynomolgus monkeys with a chimeric HIV-1/siMac virus
RT that expresses the HIV-1 envelope glycoproteins.";
RL J. Acquir. Immune Defic. Syndr. 5:639-646(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=SHIV-4, HXB2;
```

RA Reimann K.A., Li J.T., Voss G., Lekutis C., Tennen-Racz K., Racz P.,
 RA Lin W., Montefiori D.C., Lee-Parritz D.E., Lu Y., Collman R.G.,
 RA Sodroski J., Letvin N.L.,
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF041850; AAD12139.1; -
 DR EMBL: AF038399; AAB99973.1; -
 DR InterPro: IPR001831; HIV_Tat.
 DR Pfam: PF00539; Tat.1.
 DR PRINTS: PR00055; HIVTATDOMAIN.
 SO SEQUENCE 86 AA; 9837 MW; 5132A4D9796364F5 CRC64;

Query Match 90.1%; Score 429; DB 12; Length 86;
 Best Local Similarity 90.6%; Pred. No. 5.2e-43;
 Matches 77; Conservative 1; Mismatches 5; Indels 2; Gaps 1;

OY 1 EPVDPRLPMPKHPGSOPTACTNCYCKKCCFHCQVCFITK--AISYGRKRORRRPQG 58
 DB 2 EPVDPRLPMPKHPGSOPTACTNCYCKKCCFHCQVCFITKLGISYGRKRORRRAPQD 61

OY 59 SOTHQVSLSKOPTSOSRGDPTGPKE 83
 DB 62 SOTHQVSLSKOPTSOSRGDPTGPKE 86

RESULT 6

O9DHA9 PRELIMINARY; PRT; 101 AA.

AC O9DHA9; PRT; 101 AA.
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE TAT PROTEIN.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 NC NCB1_TaxID=11676;
 RN [1]
 RP MEDLINE=20457217; PubMed=11000225;
 RX Yuste E., Lopez-Galindez C., Domingo E.;
 RA "Unusual Distribution of Mutations Associated with Serial Bottleneck
 RT Passages of Human Immunodeficiency Virus Type 1.";
 RL J. Virol. 74:9546-9552(2000).
 RL EMBL: AF256210; AAG16839.1; -
 DR EMBL: AF256209; AAG16831.1; -
 DR InterPro: IPR001831; HIV_Tat.
 DR Pfam: PF00539; Tat.1.
 DR PRINTS: PR00055; HIVTATDOMAIN.
 SO SEQUENCE 101 AA; 11425 MW; 1A1EA5C93960630E CRC64;

Query Match 90.1%; Score 429; DB 12; Length 101;
 Best Local Similarity 90.6%; Pred. No. 5.9e-43;
 Matches 77; Conservative 0; Mismatches 6; Indels 2; Gaps 1;

OY 1 EPVDPRLPMPKHPGSOPTACTNCYCKKCCFHCQVCFITK--AISYGRKRORRRPQG 58
 DB 2 EPVDPRLPMPKHPGSOPTACTNCYCKKCCFHCQVCFITKLGISYGRKRORRRAPQD 61

OY 59 SOTHQVSLSKOPTSOSRGDPTGPKE 83
 DB 62 SOTHQVSLSKOPTSOSRGDPTGPKE 86

RESULT 7

O99BV6 PRELIMINARY; PRT; 86 AA.

AC O99BV6; PRT; 86 AA.
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE TAT PROTEIN.
 GN TAT.

OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 NC NCB1_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=pg.3;
 RA Aldous M.C., Schwager M., Mok J.Y.O., Yirrell D.L., Leigh Brown A.J.,
 RA Froebel K.S.;
 RT "The natural history of pediatric HIV infection suggests an
 RT association between the specificity of the cytotoxic T cells and
 RT clinical outcome.";
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF324447; AAK14289.1; -
 SO SEQUENCE 86 AA; 9726 MW; 276EB488E3291174 CRC64;

Query Match 89.7%; Score 427; DB 12; Length 86;
 Best Local Similarity 90.6%; Pred. No. 8.9e-43;
 Matches 77; Conservative 0; Mismatches 6; Indels 2; Gaps 1;

OY 1 EPVDPRLPMPKHPGSOPTACTNCYCKKCCFHCQVCFITK--AISYGRKRORRRPQG 58
 DB 2 EPVDPRLPMPKHPGSOPTACTNCYCKKCCFHCQVCFITKLGISYGRKRORRRAPQD 61

OY 59 SOTHQVSLSKOPTSOSRGDPTGPKE 83
 DB 62 SOTHQVSLSKOPTSOSRGDPTGPKE 86

RESULT 8

O99BV3 PRELIMINARY; PRT; 86 AA.

AC O99BV3; PRT; 86 AA.
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE TAT PROTEIN.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 NC NCB1_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=P12.3;
 RA Aldous M.C., Schwager M., Mok J.Y.O., Yirrell D.L., Leigh Brown A.J.,
 RA Froebel K.S.;
 RT "The natural history of pediatric HIV infection suggests an
 RT association between the specificity of the cytotoxic T cells and
 RT clinical outcome.";
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF324450; AAK14292.1; -
 SO SEQUENCE 86 AA; 9792 MW; 30CDFA726F910F2 CRC64;

Query Match 89.7%; Score 427; DB 12; Length 86;
 Best Local Similarity 89.4%; Pred. No. 8.9e-43;
 Matches 76; Conservative 1; Mismatches 6; Indels 2; Gaps 1;

OY 1 EPVDPRLPMPKHPGSOPTACTNCYCKKCCFHCQVCFITK--AISYGRKRORRRPQG 58
 DB 2 EPVDPRLPMPKHPGSOPTACTNCYCKKCCFHCQVCFITKLGISYGRKRORRRAPQD 61

OY 59 SOTHQVSLSKOPTSOSRGDPTGPKE 83
 DB 62 SOTHQVSLSKOPTSOSRGDPTGPKE 86

RESULT 9

O99BV7 PRELIMINARY; PRT; 101 AA.

AC O99BV7; PRT; 101 AA.
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
DE TAT PROTEIN.
CN TAT.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=P.2;
RA Aldous M.C., Schwager M., Mok J.Y.Q., Virrell D.L., Leigh Brown A.J.,
RT Froebel K.S.;
RT "The natural history of pediatric HIV infection suggests an
RT association between the specificity of the cytotoxic T cells and
RT clinical outcome."
RL Submitted (NOV-2000) to the EMBL/genbank/DBJ databases.
DR EMBL: AF324446; AAK14288.1; -
SQ SEQUENCE 101 AA; 11517 MW; 03AB48CC28C9DE2 CRC64;

Query Match 89.7%; Score 427; DB 12; Length 101;
Best Local Similarity 90.6%; Pred. No. 1e-42;
Matches 77; Conservative 0; Mismatches 6; Indels 2; Gaps 1;

OY 1 EPVDPRLPEPMKHPGSOPTACTNCYCKKCCFHQVCFTK--AISYGRKKRRRRPPG 58
|||||
DB 2 EPVDPRLPEPMKHPGSOPTACTNCYCKKCCFHQVCFTKGLGISYGRKKRRRRPPG 61
OY 59 SOTHQVSLSKOPTSOSRGDPTGPKE 83
|||||
DB 62 SOTHQVSLSKOPTSOSRGDPTGPKE 86

RESULT 10
O99BWL PRELIMINARY; PRT; 86 AA.
ID O99BWL
AC O99BWL;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
DE TAT PROTEIN.
GN TAT.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=P.2;
RA Aldous M.C., Schwager M., Mok J.Y.Q., Virrell D.L., Leigh Brown A.J.,
RT Froebel K.S.;
RT "The natural history of pediatric HIV infection suggests an
RT association between the specificity of the cytotoxic T cells and
RT clinical outcome."
RL Submitted (NOV-2000) to the EMBL/genbank/DBJ databases.
DR EMBL: AF324440; AAK14283.1; -
SQ SEQUENCE 86 AA; 9725 MW; 3A1C9D514983A7A8 CRC64;

Query Match 89.5%; Score 426; DB 12; Length 86;
Best Local Similarity 89.4%; Pred. No. 1.2e-42;
Matches 76; Conservative 1; Mismatches 6; Indels 2; Gaps 1;

OY 1 EPVDPRLPEPMKHPGSOPTACTNCYCKKCCFHQVCFTK--AISYGRKKRRRRPPG 58
|||||
DB 2 EPVDPRLPEPMKHPGSOPTACTNCYCKKCCFHQVCFTKGLGISYGRKKRRRRPPG 61
OY 59 SOTHQVSLSKOPTSOSRGDPTGPKE 83
|||||
DB 62 SOTHQVSLSKOPTSOSRGDPTGPKE 86

RESULT 11
O99BWO PRELIMINARY; PRT; 86 AA.

AC O99BWO;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
DE TAT PROTEIN.
CN TAT.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=P.1;
RA Aldous M.C., Schwager M., Mok J.Y.Q., Virrell D.L., Leigh Brown A.J.,
RT Froebel K.S.;
RT "The natural history of pediatric HIV infection suggests an
RT association between the specificity of the cytotoxic T cells and
RT clinical outcome."
RL Submitted (NOV-2000) to the EMBL/genbank/DBJ databases.
DR EMBL: AF324442; AAK14285.1; -
SQ SEQUENCE 86 AA; 9803 MW; 9B0D8E524AEC1B0E CRC64;

Query Match 89.5%; Score 426; DB 12; Length 86;
Best Local Similarity 90.6%; Pred. No. 1.2e-42;
Matches 77; Conservative 0; Mismatches 6; Indels 2; Gaps 1;

OY 1 EPVDPRLPEPMKHPGSOPTACTNCYCKKCCFHQVCFTK--ISYGRKKRRRRPPG 58
|||||
DB 2 EPVDPRLPEPMKHPGSOPTACTNCYCKKCCFHQVCFTKGLGISYGRKKRRRRPPG 61
OY 59 SOTHQVSLSKOPTSOSRGDPTGPKE 83
|||||
DB 62 SOTHQVSLSKOPTSOSRGDPTGPKE 86

RESULT 12
O9DH20 PRELIMINARY; PRT; 101 AA.
ID O9DH20
AC O9DH20;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
DE TAT PROTEIN.
GN TAT.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20457217; PubMed=11000225;
RA Yuste E., Lopez-Galindez C., Domingo E.;
RT "Unusual distribution of mutations associated with serial Bottleneck
RT passages of Human Immunodeficiency Virus Type 1."
RL J. Virol. 74:9546-9552(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Yuste E., Lopez-Galindez C., Domingo E.;
RL Submitted (APR-2000) to the EMBL/genbank/DBJ databases.

DR EMBL: AF256211; AAG16848.1; -
DR EMBL: AF256204; AAG16788.1; -
DR EMBL: AF256205; AAG16797.1; -
DR EMBL: AF256206; AAG16805.1; -
DR EMBL: AF256207; AAG16814.1; -
DR EMBL: AF256208; AAG16822.1; -
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat; 1.
DR PRINTS: PR00055; HIVTATDOMAIN.
SQ SEQUENCE 101 AA; 11453 MW; 831E576C7E82C649 CRC64;

Query Match 89.5%; Score 426; DB 12; Length 101;
Best Local Similarity 89.4%; Pred. No. 1.3e-42;
Matches 76; Conservative 1; Mismatches 6; Indels 2; Gaps 1;

OY	1	EPVDRLEPMHPSOPACTACTNCYCKKCCFHCOVCFTTK--AISYGKKRRRRRRPOG	58
Db	2	EPVDRLEPMHPSOPACTACTNCYCKKCCFHCOVCFTTGLGISYGKKRRRRRAPOD	61
OY	59	SQTHQVSLSKQPTSGRSRCDPTGPKE	83
Db	62	SQTHQVSLSKQPASQPGDPTGPKE	86
RESULT	13		
ID	056318	PRELIMINARY;	PRT; 101 AA.
AC	056318		
DT	01-JUN-1998	(TREMBLrel. 06, Created)	
DT	01-JUN-1998	(TREMBLrel. 06, Last sequence update)	
DT	01-JUN-2001	(TREMBLrel. 17, Last annotation update)	
DE	STRAIN SHIV-89.6, COMPLETE GENOME.		
GN	TAT.		
OS	Simian immunodeficiency virus.		
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.		
OX	NCBI_TaxID=57667;		
RN	11		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-SHIV-89.6;		
RX	MEDLINE=96186751; PubMed=8627800;		
RA	Reimann K.A., Li J.T., Voss G., Lekutis C., Tenner-Racz K., Racz P.,		
RA	Lin W., Montefiori D.C., Lee-Parritz D.E., Lu Y., Collman R.G.,		
RA	Sodroski J., Lelevin N.L.;		
RT	"An env gene derived from a primary human immunodeficiency virus type		
RT	1 isolate confers high in vivo replicative capacity to a chimeric		
RL	simian/human immunodeficiency virus in rhesus monkeys."		
RN	J. Virol. 70:3198-3206(1996).		
RP	121		
RC	SEQUENCE FROM N.A.		
RC	STRAIN-SHIV-89.6;		
RA	Reimann K.A., Li J.T., Voss G., Lekutis C., Tenner-Racz K., Racz P.,		
RA	Lin W., Montefiori D.C., Lee-Parritz D.E., Lu Y., Collman R.G.,		
RL	Sodroski J., Lelevin N.L.;		
DR	Submitted (DEC-1997) to the EMBL/Genbank/DBJ databases.		
DR	EMBL: AF038398; AAB99963.1;		
DR	InterPro: IPR001831; HIV_Tat.		
DR	Pfam: Pf00539; Tat. 1.		
DR	PRINTS: PR00055; HIVTATDOMAIN.		
SO	SEQUENCE 101 AA; 11629 MW; ACC85C209970DDE9 CRC64;		
Query Match	89.3%;	Score 425;	DB 12; Length 101;
Best Local Similarity	89.4%;	Pred. No. 1.7e-42;	
Matches	76;	Conservative	2; Mismatches 5; Indels 2; Gaps 1;
OY	1	EPVDRLEPMHPSOPACTACTNCYCKKCCFHCOVCFTTKA--ISYGKKRRRRRRPOG	58
Db	2	EPVDRLEPMHPSKPTACTACTNCYCKKCCFHCOVCFTTGLGISYGKKRRRRRAHON	61
OY	59	SQTHQVSLSKQPTSGRSRCDPTGPKE	83
Db	62	SQTHQVSLSKQPSQPGDPTGPKE	86
RESULT	14		
ID	092885	PRELIMINARY;	PRT; 101 AA.
AC	092885		
DT	01-NOV-1998	(TREMBLrel. 08, Created)	
DT	01-NOV-1998	(TREMBLrel. 08, Last sequence update)	
DT	01-JUN-2001	(TREMBLrel. 17, Last annotation update)	
DE	TAT PROTEIN.		
GN	TAT.		
OS	Human immunodeficiency virus type 1.		
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.		
OX	NCBI_TaxID=11676;		
RN	11		
RP	SEQUENCE FROM N.A.		

RC	STRAIN=MC925;
RA	Oelrichs R.B.; McPhee D.A.; Deacon N.J.:
RT	"Biological cloning and full-length sequence of two Australian HIV-1
RT	primary clinical isolates with distinct cellular tropism and
RT	cytopathicity."
RL	Submitted (JAN-1998) to the EMBL/GenBank/DBDJ databases.
DR	EMBL; AF042101; AAD03203.1; "-
DR	InterPro: IPR001831; HIV_Tat.
DR	Pfam; PF00539; Tat; 1.
DR	PRINTS; PRO0055; HIVTATDOMAIN.
SQ	SEQUENCE 101 AA; 11576 MW; 933522537923FBD CRC64;

Query Match	89.3%;	Score 425;	DB 12;	Length 101;
Best Local Similarity	89.4%;	Pred. No. 1.7e-42;		
Matches 76;	Conservative 1;	Mismatches 6;	Indels 2;	Gaps 1;

Oy	1	EEVDRLPEPMWHPGSOPTACTACTCYCKKCCCFHCQVCFTTKA--ISYGRKKRRQRPPQG	58
Dd	2	EFDVRLPEPMWHPGSOPTACTPCYCCKCFCFCQVCFTTKAGIISTYGKRKKRORRRAPQN	61
Oy	59	SOTHOVSLSKOPTOSRGDPTPKKE	83
Dd	62	SOTHOVSLSKOPASOPRGDPAGEKE	86

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RESULT 15
092899
ID 092899 PRELIMINARY; PRT: 101 AA.
AC 092899;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE TAT PROTEIN.
GN TAT.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCD36;
RA Geirichs R.B., McPhee D.A., Deacon N.J.;
RT "Genomic sequence of HIV-1 from four members of the Sydney Blood Bank
RT Cohort of long term non-progressors.";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF042105; AAD03236.1; -
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat: 1.
DR PRINTS: PR00055; HIVTATDOMAIN.
SO SEQUENCE 101 AA; 11512 MW; 440B807DAF4873BE CRC64;

Query Match 89.3%; Score 425; DB 12; Length 101;
Best Local Similarity 87.1%; Pred. No. 1.7e-42;
Matches 74; Conservative 5; Mismatches 4; Indels 2; Gaps 1;

QY 1 EPVDRLEPMKIPGSGQPKACTNCYCKCKCCFCQCYFITK--AISYGRKKRRORRRPPG 58
DB 2 EYVDRLEPMKIPGSGQPKACTSCYCKCKCCFCQCYFITKGLGISGSKRRORRRPPD 61
QY 59 SOTHQVSLSKQPTSSQRCGDPGPK 83
DB 62 NQTHQVSLSKQPSQRCGDPGPK 86

Search completed: January 10, 2002, 15:35:44
Job time: 102 sec

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Thu Jan 10 15:38:07 2002

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